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L5 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2002 ACS
2001:333513 Document No. 135:370654 Human and mouse **anergy**
associated genes **GRAIL**. Ford, Gregory S.; Bloom, Debra;
Fathman, C. Garrison (The Board of Trustees of the Leland Stanford Junior
University, USA). ECT Int. Appl. WO 1991095943 A1 20011115, 50 pp.
DESIGNATED STATES: W: AU, CA, JP; BW: AT, BE, CH, CY, DE, DK, ES, FI, FR,
GB, GR, IE, IT, LU, MC, NL, PT, SE, TR. (English). CODEN: PIXXD2.
APPLICATION: WO 2001-US15365 20010511. PRIORITY: US 2000-PV203513
20000511.

AB Isolated nucleic acid compns. and sequences of **anergy** assocd.
genes are provided, including the novel **GRAIL** gene. Expression
of these genes is unregulated during the early stages of induction of
anergy. The murine **GRAIL** sequence is shown to attenuate
IL-2 transcription in T cells during response to antigenic stimulation.
The identification of genes involved in the induction of **anergy**
is useful in the evaluation of the pathophysiol. or immunotherapy of

cancer, autoimmune disease, and transplant rejection. Genetic sequences involved in **anergy** induction are useful markers in the evaluation of specific immunotherapies. Functional characterization of genes involved in **anergy** induction allows the elucidation of the mechanism(s) of T cell **anergy**, including the transcriptional blockade of IL-2, which may be manipulated to regulate T cell responses in human disease. The signaling pathways involving **GRAIL** are of significant interest in the identification of drugs that either block or upregulate the function(s) of **GRAIL**.

L5 ANSWER 2 OF 2 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V. DUPLICATE 1
2001361386 EMBASE CD4(+)CD25(+) T cells facilitate the induction of T cell
anergy. Ermann J.; Szanya V.; Ford G.S.; Paragas V.; Fathman C.G.;
Lejon K.; Dr. C.G. Fathman, Stanford University Sch. of Med., Ctr. for
Clinical Sci. Res. Bldg., 390 Pasteur Drive, Stanford, CA 94305-5166,
United States. cfathman@stanford.edu. Journal of Immunology 167/8
(4271-4275) 15 Oct 2001.

Refs: 23.

ISSN: 0022-1767. CODEN: JOIMA3. Pub. Country: United States. Language:
English. Summary Language: English.

AB T cell **anergy** is characterized by the inability of the T cell to
produce IL-2 and proliferate. It is reversible by the addition of
exogenous IL-2. A similar state of unresponsiveness is observed when the
proliferative response of murine CD4(+)CD25(-) T cells is suppressed in
vitro by coactivated CD4(+)CD25(+) T cells. We have developed a
suppression system that uses beads coated with anti-CD3 and anti-CD28 Abs
as surrogate APCs to study the interaction of CD4(+)CD25(+) and
CD4(+)CD25(-) T cells in vitro. CD4(+)CD25(+) T cell-induced suppression,
in this model, was not abrogated by blocking the B7-CTLA-4 pathway. When
the CD4(+)CD25(-) T cells were separated from the CD4(+)CD25(+) suppressor
cells after 24 h of coactivation by the Ab-coated beads, the CD4(+)CD25(-)
T cells were unable to proliferate or to produce IL-2 upon restimulation.
The induction of this anergic phenotype in the CD4(+)CD25(-) T cells
correlated with the up-regulated expression of the gene related to
anergy in lymphocytes (**GRAIL**), a novel **anergy**
-related gene that acts as a negative regulator of IL-2 transcription.
This system constitutes a novel mechanism of **anergy** induction in
the presence of costimulation.

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L7 62 L6 AND ANERGY

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L8 30 DUF REMOVE L7 (39 DUPLICATES REMOVED)

=> d 18 1-30 cbik abs

L5 ANSWER 1 OF 30 CAFLUS COPYRIGHT 2002 ACS
2001:533513 Document No. 139:370654 Human and mouse **anergy**
associated genes **GRAIL**. Ford, Gregory S.; Bloom, Debra
; Fathman, C. Garrison (The Board of Trustees of the Leland
Stanford Junior University, USA). PCT Int. Appl. WO 2001085943 A1
20011111, 50 pp. DESIGNATED STATES: W: AU, CA, JP; RW: AT, BE, CH, CY,
DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TH. (English).
CODEN: PIXXD1. APPLICATION: WO 2001-US19385 20010511. PRIORITY: US
2000-PV203513 20000511.

AB Isolated nucleic acid compns. and sequences of **anergy** assocd.
genes are provided, including the novel **GRAIL** gene. Expression of these

genes is unregulated during the early stages of induction of **anergy**. The murine GRAIL sequence is shown to attenuate IL-2 transcription in T cells during response to antigenic stimulation. The identification of genes involved in the induction of **anergy** is useful in the evaluation of the pathophysiol. or immunotherapy of cancer, autoimmune disease, and transplant rejection. Genetic sequences involved in **anergy** induction are useful markers in the evaluation of specific immunotherapies. Functional characterization of genes involved in **anergy** induction allows the elucidation of the mechanism(s) of T cell **anergy**, including the transcriptional blockade of IL-2, which may be manipulated to regulate T cell responses in human disease. The signaling pathways involving GRAIL are of significant interest in the identification of drugs that either block or upregulate the function(s) of GRAIL.

- L8 ANSWER 2 OF 30 MEDLINE DUPLICATE 1
 2001544740 Document Number: 21475847. PubMed ID: 11591742. CD4(+)CD25(+) T cells facilitate the induction of T cell **anergy**. Ermann J; Spanya V; Ford G S; Paragas V; Fathman C G; Lejon K. (Division of Immunology and Rheumatology, Department of Medicine, Stanford University School of Medicine, Stanford, CA 94305, USA.) JOURNAL OF IMMUNOLOGY, (2001 Oct 15) 167 (8) 4271-5. Journal code: 2985117R. ISSN: 0022-1767. Pub. country: United States. Language: English.
- AB T cell **anergy** is characterized by the inability of the T cell to produce IL-2 and proliferate. It is reversible by the addition of exogenous IL-2. A similar state of unresponsiveness is observed when the proliferative response of murine CD4(+)CD25(-) T cells is suppressed in vitro by coactivated CD4(+)CD25(+) T cells. We have developed a suppression system that uses beads coated with anti-CD3 and anti-CD28 Abs as surrogate APCs to study the interaction of CD4(+)CD25(+) and CD4(+)CD25(-) T cells in vitro. CD4(+)CD25(+) T cell-induced suppression, in this model, was not abrogated by blocking the B7-CTLA-4 pathway. When the CD4(+)CD25(-) T cells were separated from the CD4(+)CD25(+) suppressor cells after 24 h of coactivation by the Ab-coated beads, the CD4(+)CD25(-) T cells were unable to proliferate or to produce IL-2 upon restimulation. The induction of this anergic phenotype in the CD4(+)CD25(-) T cells correlated with the up-regulated expression of the gene related to **anergy** in lymphocytes (GRAIL), a novel **anergy**-related gene that acts as a negative regulator of IL-2 transcription. This system constitutes a novel mechanism of **anergy** induction in the presence of costimulation.

- L8 ANSWER 3 OF 30 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
 2001:41086 Document No.: PREVIEW00041086. Identification and functional characterization of a novel gene which is upregulated in anergic T cells. Ford, G. S. (1); Ermann, J. (1); Paragas, V. (1); Bloom, D. (1); Fathman, C. G. (1). (1) Stanford University School of Medicine, Palo Alto, CA USA. FASEB Journal, (April 28, 2000) Vol. 14, No. 6, pp. A1216. print. Meeting Info.: Joint Annual Meeting of the American Association of Immunologists and the Clinical Immunology Society Seattle, Washington, USA May 12-16, 2000 ISSN: 0893-6633. Language: English. Summary Language: English.

- L8 ANSWER 4 OF 30 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
 2001:210541 Document No.: PREVIEW000210541. CD4+CD25+ cells: Facilitators of T cell **anergy**. Ermann, J. (1); Lejon, K.; Ford, G. (1); Fathman, C. G. (1). (1) Department of Medicine, Stanford University School of Medicine, Stanford, CA USA. Immunobiology, (November, 2000) Vol. 203, No. 1-2, pp. 194-195. print. Meeting Info.: Joint Annual Meeting of the German and Dutch Societies of Immunology Dusseldorf, Germany November 29-December 02, 2000 ISSN: 0171-2985. Language: English. Summary Language: English.

L8 ANSWER 5 OF 30 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE
2

2002:106933 Document No.: PREV200200106933. **Anergy** genes.
Bloom, D.; Fathman, C. G.; Slaymaker, S.. Mountain View,
Calif. USA. ASSIGNEE: THE BOARD OF TRUSTEES OF THE LELAND STANFORD JUNIOR
UNIVERSITY. Patent Info.: US 5747299 May 5, 1998. Official Gazette of the
United States Patent and Trademark Office Patents, (May 5, 1998) Vol.
1210, No. 1, pp. 451. ISSN: 0098-1133. Language: English.

L8 ANSWER 6 OF 30 SCISEARCH COPYRIGHT 2002 ISI (R)
1998:775748 The Genuine Article (R) Number: 121HD. The induction of T
lymphocyte **anergy**: Ras dependence and IL-2 transcription
revisited. **Bloom D D (Reprint)**; Yang Y; Moore E B; **Fathman**
C G. STANFORD UNIV, SCH MED, STANFORD, CA 94305. FASEB JOURNAL (20
MAR 1998) Vol. 12, No. 5, Part 2, Supp. [S], pp. 5378-5378. Publisher:
FEDERATION AMER SOC EXP BIOL. 3610 ROCKVILLE PIKE, BETHESDA, MD 20814-3998
. ISSN: 0892-6636. Pub. country: USA. Language: English.

L8 ANSWER 7 OF 30 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
1998:103756 Document No.: PREV199806103756. The induction of T lymphocyte
anergy: Ras dependence and IL-2 transcription revisited.
Bloom, Debra D.; Yang, Yang; Moore, Bethany B.; **Fathman, C.**
Garrison. Stanford Univ. Sch. Med., Stanford, CA 94305 USA. FASEB
Journal, (March 20, 1998) Vol. 12, No. 5, pp. A929. Meeting Info.: Annual
Meeting of the Professional Research Scientists on Experimental Biology
98, Part II San Francisco, California, USA April 18-22, 1998 Federation of
American Societies for Experimental Biology. ISSN: 0892-6638. Language:
English.

L8 ANSWER 8 OF 30 SCISEARCH COPYRIGHT 2002 ISI (R)
1998:628555 The Genuine Article (R) Number: 109UX. Prolongation of cardiac
graft survival with anti-CD4Ig plus hCTLA4Ig in primates. Krieger N R;
Yuh D; McIntyre W B; Flavin T F; Yin D P; Robbins R; **Fathman C G**
(Reprint). STANFORD UNIV, MED CTR, SCH MED, DEPT MED, DIV IMMUNOL &
RHEUMATOL, ROOM 3-021, STANFORD, CA 94305 (Reprint); STANFORD UNIV, MED
CTR, SCH MED, DEPT MED, DIV IMMUNOL & RHEUMATOL, STANFORD, CA 94305;
STANFORD UNIV, MED CTR, DIV IMMUNOL, STANFORD, CA 94305. JOURNAL OF
SURGICAL RESEARCH (MAY 1998) Vol. 76, No. 3, pp. 174-178. Publisher:
ACADEMIC PRESS INC JNL-COMP SUBSCRIPTIONS. 505 B ST, STE 1900, SAN DIEGO,
CA 92101-4495. ISSN: 0012-4804. Pub. country: USA. Language: English.
ABSTRACT IS AVAILABLE IN THE ALL JNL IALL FORMATS

AB Background The aim of this study was to determine whether the use of
combined immunotherapy with a brief course of humanized anti-CD4Ig and
hCTLA4Ig would prolong heterotopic cardiac allograft survival in primates
(rhesus monkeys). This model was based on work in "high responder" rats
where a brief course of depletive anti-CD4 mAb plus hCTLA4Ig was
successful in inducing transplantation tolerance.

Methods. Heterotopic cardiac transplants were performed in rhesus
recipients. Donor/recipient pairs between groups were confirmed to be
reactive prior to transplantation by MLC matching. Humanized anti-CD4Ig, a
recently developed anti-CD4 mAb, was given at a dose of 20 mg/kg i.v. on
days -3, -2, -1, and 0. hCTLA4Ig was administered at 6 mg/kg/dose i.v. on
days 0 and 2 for the first recipient and days 0, 2, 4, and 6 for the
second recipient. No further immunosuppression was administered. The
treated (n = 2) or untreated (n = 5) recipients were followed for graft
function by daily palpitation.

Results. Treatment with anti-CD4Ig plus hCTLA4Ig resulted in a
significant prolongation of heart graft survival (42 days for the first
recipient and 52 days for the second recipient) compared to untreated
recipients (7 days x 4, 11 days x 1). FACS analysis demonstrated CD4
depletion of anti-CD4 treated animals to <2% on posttransplant day 1. The
CD4(+) T cells gradually repopulated to 50-70% pretransplant levels just
prior to rejection. No adverse responses (fever, tachypnea, tachycardia,

infections) were observed.

Conclusions. These are the first results demonstrating that a brief course of combined specific induction immunotherapy with humanized anti-CD4Ig plus hCTLA4Ig, in the absence of adjuvant posttransplant immunosuppression, was well tolerated and resulted in marked prolongation of cardiac allograft survival in primates. (C) 1998 Academic Press.

L8 ANSWER 9 OF 30 SCISEARCH COPYRIGHT 2002 ISI (R)

1998:362990 The Genuine Article (R) Number: 2L990. Th1 unresponsiveness can be infectious for unrelated antigens. Charlton B (Reprint); **Fathman C G**; Slattery R M. AUSTRALIAN NATL UNIV, JOHN CURTIN SCH MED RES, CANBERRA, ACT 2601, AUSTRALIA (Reprint); STANFORD UNIV, MED CTR, DEPT MED, DIV RHEUMATOL & IMMUNOL, SCH MED, STANFORD, CA 94305. IMMUNOLOGY AND CELL BIOLOGY (APR 1998) Vol. 76, No. 2, pp. 173-178. Publisher: BLACKWELL SCIENCE. 54 UNIVERSITY ST, P O BOX 378, CARLTON VICTORIA 3053, AUSTRALIA. ISSN: 0818-2641. Pub. country: AUSTRALIA; USA. Language: English.
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB CD4(+) T cells may be assigned a functional status (Th1 or Th2) according to the cytokines they produce including IL-2, IFN-gamma and IL-4. Th1 and Th2 CD4(+) T cells deliver different isotype-switching signals to antigen-specific B cells which bias the serum Ig isotypes. The stimulation of Th1 or Th2 responses is influenced by adjuvants and administration of antigen in IFA results in Th1 unresponsiveness as evidenced by: (i) reduced T cell proliferation to antigen; (ii) reduced IFN-gamma production in response to antigen; and (iii) reduced IgG2a isotype antigen-specific antibodies following antigen/CFA challenge. The impact of established human gamma globulin (HGG) specific Th1 unresponsiveness on subsequent immunization with an unrelated antigen, human serum albumin (HSA) in Th1-inducing CFA was then examined. When subsequently challenged with a mixture of HSA and HGG in CFA the HGG-specific Th1 unresponsiveness was infectious and dominant, preventing the induction of a Th1 response to HSA. Reduced T cell proliferation, IFN-gamma production and IgG2a antibody were consequently observed in response to HSA. The HGG-specific Th1 unresponsiveness was not infectious when HGG/CFA and HSA/CFA were administered at separate sites. This demonstrates that antigen-specific Th1 unresponsiveness can be infectious for new, molecularly unrelated antigens and supports studies showing that Th1-mediated autoimmune diseases such as experimental allergic encephalomyelitis (EAE) and diabetes can be ameliorated using antigens molecularly distinct from the disease-inducing immunogen.

L8 ANSWER 10 OF 30 SCISEARCH COPYRIGHT 2002 ISI (R)

1998:569627 The Genuine Article (R) Number: 101VR. Anti-CD4 therapy in combined heart-kidney, heart-liver, and heart small bowel allotransplants in high-responder rats. Yin D F (Reprint); Sankary H H; TalorEdwards C; Chong A S F; Foster P; Shen J K; Ma L D; Williams J W; **Fathman C G**. RUSH PRESBYTERIAN ST LUKES MED CTR, DEPT GEN SURG, SECT TRANSPLANTAT, 1653 W CONGRESS PKWY, CHICAGO, IL 60612 (Reprint); STANFORD UNIV, SCH MED, DEPT MED, MED CTR, DIV IMMUNOL, STANFORD, CA 94305. TRANSPLANTATION (15 JUL 1998) Vol. 66, No. 1, pp. 1-9. Publisher: WILLIAMS & WILKINS. 351 WEST CAMDEN ST, BALTIMORE, MD 21201-2436. ISSN: 0041-1337. Pub. country: USA. Language: English.
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Background. In these experiments, we studied the role of anti-CD4 (Ox33) monoclonal antibody in the induction of allograft unresponsiveness in high-responder Lewis rats in the single liver, kidney, small bowel, and heart versus the combined heart-kidney, heart-liver, and heart-small bowel transplantation models.

Methods. ACI heart, kidney, liver, and small bowel allografts were transplanted into untreated and anti-CD4 treated Lewis rats. In selected animals bearing long-surviving ACI liver or kidney allografts for over 3 months, donor-matched second heart or third-party (Brown Norway) heart allografts were transplanted. Simultaneously, heart-liver, heart-kidney,

and heart-small bowel transplants were performed on the day of operation. Rejected allografts were verified by autopsy and pathology.

Results. ACI liver allografts were permanently accepted by Lewis recipients treated with either regular-dose (5 mg/kg for 4 days) or low-dose (5 mg/kg for 2 days) of anti-CD4 monoclonal antibody. Pretransplant anti-CD4 therapy (5 mg/kg for 4 days but not 5 mg/kg for 2 days) resulted in a long-term survival of kidney allografts (mean survival time [MST] >100.0 days, n=5). Pretransplant anti-CD4 treatment (5 mg/kg for 4 days) could not induce tolerance when single ACI hearts were transplanted; however, long-term survival of ACI heart allografts could be induced when heart transplants were combined with liver (n=7) or kidney (n=8) transplants. The survival of both ACI heart allografts (MST=25.0 days, n=4) and small bowel allografts (MST=28.0 days, n=4) was also prolonged when simultaneous heart and small bowel transplantation was performed in anti-CD4-treated recipients. The second ACI heart allograft was permanently accepted by tolerant Lewis recipients of ACI liver or kidney allografts induced by anti-CD4 treatment, and third-party heart grafts were acutely rejected without affecting survival of the primary allografts.

Conclusion. Our current results show that: (1) there is a vigorous rejection of heart greater than or equal to small bowel > kidney > liver in high-responder Lewis rats after pretransplant anti-CD4 therapy; and (2) simultaneous or metachronous combined liver-heart and kidney-heart transplants may protect heart allografts from rejection.

L8 ANSWER 11 OF 30 SCISEARCH COPYRIGHT 2002 ISI (R)
97:162574 The Genuine Article (R) Number: WH142. Understanding the mechanism of T lymphocyte **anergy**. **Bloom D (Reprint)**; Moore B;
Fathman C G. STANFORD UNIV, STANFORD, CA 94305. JOURNAL OF ALLERGY AND CLINICAL IMMUNOLOGY (JAN 1997) Vol. 99, No. 1, Part 2, Supp. [S], pp. 1256-1256. Publisher: MOSBY-YEAR BOOK INC. 11830 WESTLINE INDUSTRIAL DR, ST LOUIS, MO 63146-3318. ISSN: 0091-6749. Pub. country: USA. Language: English.

L8 ANSWER 12 OF 30 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
1997:144773 Document No.: PREV199799443976. Understanding the mechanism of T lymphocyte **anergy**. **Bloom, Debra**; Moore, Bethany;
Fathman, C. G. Stanford Univ., Stanford, CA USA. Journal of Allergy and Clinical Immunology, (1997) Vol. 99, No. 1 PART 2, pp. S307. Meeting Info.: Joint Meeting of the American Academy of Allergy, Asthma and Immunology, the American Association of Immunologists and the Clinical Immunology Society San Francisco, California, USA February 21-26, 1997 ISSN: 0091-6749. Language: English.

L8 ANSWER 13 OF 30 CASLUS COPYRIGHT 2002 ACS
1996:134201 Document No. 124:173452 Human gene and gene product associated with **anergy** and their diagnostic uses. **Bloom, Debra**;
Fathman, Garrison (Board of Trustees of the Leland Stanford Junior University, USA). PCT Int. Appl. WO 9600300 A1 19960104, 30 pp. DESIGNATED STATES: W: CA, JP; RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE. (English). COLEN: PIXXD2. APPLICATION: WO 1995-US7958 19950622. PRIORITY: US 1994-265100 19940623.

AB Genes assocd. with the induction of **anergy** in T-cells and methods of detecting them and the use of the genes or proteins as diagnostics for monitoring induction of tolerance for the presence of tolerized T-cells in a physiol. sample, or elucidating the pathway to **anergy** or activation in T-cells are described. A cysteine string protein is found to indicate quiescent T-cells and is lost with anergic T-cells. cDNAs assocd. with **anergy** were cloned from an anergic T-cell clone by differential display.

L8 ANSWER 14 OF 30 SCISEARCH COPYRIGHT 2002 ISI (R)
96:277058 The Genuine Article (R) Number: UE192. QUANTITATIVE-ANALYSIS OF

T-CELL ACTIVATION - ROLE OF TCR LIGAND DENSITY AND TCR AFFINITY. KIM D T; ROTHBARD J B; **BLOOM D D; FATHMAN C G (Reprint)**. STANFORD UNIV, SCH MED, DEPT MED, DIV RHEUMATOL & IMMUNOL, STANFORD, CA, 94305 (Reprint); STANFORD UNIV, SCH MED, DEPT MED, DIV RHEUMATOL & IMMUNOL, STANFORD, CA, 94305. JOURNAL OF IMMUNOLOGY (15 APR 1996) Vol. 156, No. 8, pp. 2737-2742. ISSN: 0022-1767. Pub. country: USA. Language: ENGLISH.

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB (B6xA)F-1 mice were immunized with sperm whale myoglobin, and T cell clones and hybridomas were generated. Hybridoma 74a.e9 was specific for the sperm whale myoglobin 67-79 peptide and could be partially activated by a peptide analogue, equine myoglobin with a natural 74G substitution. Using this hybridoma in T cell activation assays, we studied the effects of varying the avidity of the TCR for its ligand, the concentration of MHC:peptide complex in the APC, and the density of TCR on the surface. Varying ligand concentration on the surface of the APC, the TCR avidity, or the density of TCR on the T cell were equally important parameters in driving T cell activation. The mouse myoglobin (74T) analogue, however, acted as an antagonist to the T cell response. Its effectiveness was also partially determined by its ability to bind to MHC. By independently altering each of these variables and following T cell activation, we describe the interrelationships among these three components (MHC:peptide:TCR) that control the activation of the T cell.

L8 ANSWER 15 OF 30 SCISEARCH COPYRIGHT 2002 ISI (R)
95:404780 The Genuine Article (R) Number: R0619. CD4-POSITIVE SUPPRESSOR CELLS BLOCK ALLOTRANSPLANT REJECTION. YIN D P; **FATHMAN C G (Reprint)**. STANFORD UNIV, SCH MED, DIV IMMUNOL & RHEUMATOL, ROOM 3011, STANFORD, CA, 94305 (Reprint); STANFORD UNIV, SCH MED, DEPT MED, STANFORD, CA, 94305; STANFORD UNIV, SCH MED, DEPT SURG, STANFORD, CA, 94305. JOURNAL OF IMMUNOLOGY (15 JUN 1995) Vol. 154, No. 12, pp. 6339-6345. ISSN: 0022-1767. Pub. country: USA. Language: ENGLISH.

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Mechanisms of maintenance of transplantation tolerance induced in adult rats by depletive regimens of anti-CD4 before transplantation of vascularized heart allografts were studied. Despite the fact that there has been little evidence that tolerant lymphocytes could prevent allograft rejection after adoptive transfer, we demonstrated a suppressive role for lymphocytes from tolerant animals in vivo. These experiments analyzed the ability of lymphocytes from tolerant rats to protect passenger leukocyte-depleted Lewis heart grafts that had been "parked" in ACI rats (treated with pretransplant anti-CD4 and maintained for >100 days) compared with their ability to protect transplantation of fresh Lewis heart grafts in naive ACI rats. Although parked Lewis heart grafts were rejected in unmanipulated ACI recipients, parked hearts (but not naive Lewis heart allografts), were permanently accepted by naive ACI rats when syngeneic tolerant spleen cells were adoptively transferred at the time of transplantation. Further, we demonstrated that the suppressor cells in the tolerant spleen cells were CD4(+). These results suggest that CD4(+) spleen cells from tolerant rats inhibit allograft recognition and may maintain allograft tolerance by blocking the indirect pathway of allorecognition.

L8 ANSWER 16 OF 30 SCISEARCH COPYRIGHT 2002 ISI (R)
95:535015 The Genuine Article (R) Number: R0464. INDUCTION OF TOLERANCE TO HEART ALLOGRAFTS IN HIGH RESPONDER RATS BY COMBINING ANTI-CD4 WITH CTLA4IG . YIN D P; **FATHMAN C G (Reprint)**. STANFORD UNIV, SCH MED, DEPT MED, DIV IMMUNOL & RHEUMATOL, ROOM 3-021, STANFORD, CA, 94305 (Reprint); STANFORD UNIV, SCH MED, DEPT MED, DIV IMMUNOL & RHEUMATOL, STANFORD, CA, 94305. JOURNAL OF IMMUNOLOGY (15 AUG 1995) Vol. 155, No. 4, pp. 1655-1659. ISSN: 0022-1767. Pub. country: USA. Language: ENGLISH.

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB It has been difficult to induce donor-specific transplantation

tolerance in high responder Lewis rats, Results presented below demonstrate that amounts of pretransplant anti-CD4 sufficient to allow allograft tolerance in low responder strains (5 mg/kg x 4 days) did not prevent the acute rejection of ACI heart allografts in high responder Lewis recipients. Higher doses of pretransplant anti-CD4 (10 mg/kg, 15 mg/kg, and 20 mg/kg) given alone could delay but not prevent allograft rejection. Pretransplant anti-CD4 combined with anti-CD8, thymectomy, and total lymphoid irradiation all failed to produce tolerance to ACI heart allografts. However, a regimen of anti-CD4 combined with CTLA4Ig allowed indefinite survival of ACI heart allografts (mean survival time, >100 day). Second-donor matched heart grafts were permanently accepted, and third-party heart allografts were rejected by the tolerant recipients. These results suggest a new combination therapeutic strategy for clinical transplantation.

L8 ANSWER 17 OF 30 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
 1994:298453 Document No.: PREV199497298453. Mechanisms of transplantation tolerance. Charlton, Brett (1; Auchincloss, Hugh, Jr.; **Fathman, C. Garrison (1)**). (1) Stanford Univ. Sch. Med., Dep. Med., Div. Immunol. and Rheumatol., Stanford, CA 94305 USA. Paul, William E. [Editor]. Annual Review of Immunology, (1994) Vol. 12, pp. 707-734. Annual Review of Immunology. Publisher: Annual Reviews Inc. P.O. Box 10139, 4139 El Camino Way, Palo Alto, California 94306, USA. ISSN: 0732-0582. ISBN: 0-8243-3012-9. Language: English.

L8 ANSWER 18 OF 30 MEDLINE DUPLICATE 3
 95226015 Document Number: 95226015. PubMed ID: 7710719. Regulation of autoimmune response. Edgway W M; Weiner H L; **Fathman C G**. (Department of Medicine, Stanford University School of Medicine, California 94305.) CURRENT OPINION IN IMMUNOLOGY, (1994 Dec) 6 (6) 946-95. Ref: 51. Journal code: 3900118. ISSN: 0952-7915. Pub. country: ENGLAND: United Kingdom. Language: English.

AB Recent work on such apparently disparate fields as T-cell receptor peptide-induced regulation, superantigens, antigen-induced tolerance, models of peripheral tolerance, apoptosis, and T-cell receptor antagonists demonstrates a similarity in immune response from a regulatory perspective. In many systems, a 'tolerance' pathway is observed, characterized broadly as an initial disturbance in the immune system, with a resulting predominance of effector cells, followed by a homeostatic response (often requiring CD8+ cells) which leads the effector population into T-cell receptor downregulation, T-cell inactivation, **anergy** and, often, eventual apoptotic death. In the regulated immune response, mixed populations of anergized and apoptosing T cells can be found. In some cases, **anergy** appears to lead to death while, in other instances, cells revert to a functional state. This review focuses on recent papers examining each of these topics in an attempt to obtain a preliminary integrated picture of immune regulation in autoimmune diseases.

L8 ANSWER 19 OF 30 MEDLINE DUPLICATE 4
 94280734 Document Number: 94280734. PubMed ID: 8011295. Mechanisms of transplantation tolerance. Charlton B; Auchincloss H Jr; **Fathman C G**. (Stanford University School of Medicine, Department of Medicine, California 94305.) ANNUAL REVIEW OF IMMUNOLOGY, (1994) 12 707-34. Ref: 216. Journal code: 3309204. ISSN: 0732-0582. Pub. country: United States. Language: English.

AB Transplantation tolerance, the long-term acceptance of grafted tissue in the absence of continuous immunosuppression, remains an elusive goal in humans, but it has been achieved in animal models using numerous approaches. The mechanisms behind graft acceptance vary according to the means used to create the state of acceptance. Several major mechanisms can now be recognized. While thymic deletion of T cells appears to be a mainstay of self-tolerance, its role in transplantation tolerance now

seems to be less significant. In contrast, extrathymic mechanisms of transplantation tolerance seem to be major factors in long-term graft acceptance. If donor antigens are presented in a nonimmunogenic manner on the graft, e.g. due to modification of graft tissue by culture, peripheral T cells of the recipient may ignore the graft. Alternatively, nonstimulatory presentation of donor antigens on graft tissue can induce a state of unresponsiveness in recipient T cells, i.e. **anergy**, rather than activating them to destroy the graft. Suppression mechanisms also operate to control graft rejection and may be specific or nonspecific in nature. Specific suppression mechanisms might act in an idiosyncratic or antigen-specific fashion, and evidence is accumulating that this may be mediated through the elaboration of cytokines. Donor antigen-specific T cells may be activated to produce "protective" cytokines which then regulate the generation of destructive T cells. Future therapies will be aimed at affecting graft acceptance through these peripheral mechanisms.

L8 ANSWER 20 OF 30 MEDLINE DUPLICATE 5
 95142881 Document Number: 95142881. PubMed ID: 7640850. Prevention of diabetes and insulinitis by neonatal intrathymic islet administration in NOD mice. Charlton B; Taylor-Edwards C; Tisch R; **Fathman C G**. (Department of Medicine, Stanford University Medical School CA 94305.) JOURNAL OF AUTOIMMUNITY, (1994 Oct) 7 (5) 543-60. Journal code: 8812164. ISSN: 0896-8411. Pub. country: ENGLAND: United Kingdom. Language: English.

AB The murine model of human insulin dependent diabetes mellitus (IDDM), the non-obese diabetic (NOD) mouse, develops a T cell-dependent destruction of pancreatic islets. While the target antigens are unknown, there is clearly a lack of tolerance to them. Neonatal intrathymic (i.t.) antigen injection has been successfully employed to prevent insulinitis in BB rats but previous i.t. islet antigen studies in NOD mice were done on older mice. We have injected syngeneic islets into the thymus of NOD mice at birth and found that diabetes and insulinitis can be completely prevented by this procedure. The effect is islet antigen-specific since other T cell responses, including autoimmune salivary infiltration, are unaffected. Furthermore, contrary to previous studies, cyclophosphamide administration was unable to induce diabetes in treated mice which suggests that deletion or **anergy** might be the mechanism by which neonatal intrathymic islet injection protects from disease. However, anti-islet antigen antibodies were still present in these mice which suggests that the mechanism of disease protection may be more complex.

L8 ANSWER 21 OF 30 MEDLINE DUPLICATE 6
 93203626 Document Number: 93203626. PubMed ID: 7681087. SEB induced **anergy**: modulation of immune response to T cell determinants of myoglobin and myelin basic protein. Gaur A; **Fathman C G**; Steinman L; Brocke S. (Department of Medicine, Stanford University School of Medicine, CA 94305.) JOURNAL OF IMMUNOLOGY, (1993 Apr 1) 150 (7) 3062-9. Journal code: 2985117R. ISSN: 0022-1767. Pub. country: United States. Language: English.

AB Superantigens have the ability to stimulate a subset of T cells based upon their expressed TCR beta-chain. It has been demonstrated that the administration of staphylococcal enterotoxin B (SEB) in mice leads to unresponsiveness in V beta 8+ T cells in vivo which are the same T cells that could be stimulated in vitro by this enterotoxin. We present here data on the effect of SEB administration in DBA/2 and (PL/J x SJL)F1 mice on their T cell response to two different T cell determinants, the responses against which are dominated by the use of V beta 8+ T cells. Treatment of mice with SEB not only diminished their primary T cell proliferative response to these determinants, but also was able to effectively reduce the memory T cell response. SEB treatment, however, showed only a modest effect in preventing Ac 1-11-induced experimental autoimmune encephalomyelitis in H-2u mice.

L8 ANSWER 22 OF 30 SCISEARCH COPYRIGHT 2001 ISI (F)

93:617120 The Genuine Article (R) Number: MB846. INDUCTION OF RELAPSING PARALYSIS IN EXPERIMENTAL AUTOIMMUNE ENCEPHALOMYELITIS BY BACTERIAL SUPERANTIGEN. BROCKE S (Reprint); GAUR A; PIERCY C; GAUTAM A; GIJBELS K; **FATHMAN C G**; STEINMAN L. STANFORD UNIV, MED CTR, SCH MED, DEPT NEUROL & NEUROL SCI, STANFORD, CA, 94305 (Reprint); STANFORD UNIV, MED CTR, SCH MED, DEPT MED, STANFORD, CA, 94305. NATURE (14 OCT 1993) Vol. 365, No. 6447, pp. 642-644. ISSN: 0028-0836. Pub. country: USA. Language: ENGLISH.

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB THE role of infection in the pathogenesis of clinical relapses that occur in most autoimmune diseases, including multiple sclerosis, remains to be established^{1,2}. Experimental autoimmune encephalomyelitis (EAE) serves as a model for multiple sclerosis, with episodes of relapsing paralysis³⁻⁹. In certain strains of mice, T-lymphocytes expressing the Vbeta8 T-cell receptor (TCR)6-8 engage the amino-terminal epitope Acl-11 of myelin basic protein, leading to EAE. The bacterial superantigen staphylococcal enterotoxin B (SEB) activates Vbeta8-expressing T cells. Here we show that after immunization with Acl-11, or after transfer of encephalitogenic T-cell lines or clones reactive to Acl-11, SEB induces exacerbation or relapses of paralytic disease in mice that are in clinical remission following an initial episode of paralysis, and triggers paralysis in mice with subclinical disease. Tumour necrosis factor has a critical role in the mechanism underlying SEB-induced exacerbation of disease, because anti-tumour necrosis factor antibody given in vivo delays the onset of paralysis triggered by SEB. On reactivation of autoaggressive cells through their T-cell receptor, superantigens may induce clinical relapses of autoimmune disease.

L8 ANSWER 23 OF 30 MEDLINE DUPLICATE 7
94025871 Document Number: 94025071. PubMed ID: 8212161. Evidence that clonal **anergy** is induced in thymic migrant cells after anti-CD4-mediated transplantation tolerance. Alters S E; Song H K; **Fathman C G**. (Department of Medicine, Stanford University School of Medicine, California 94305-5111. : TRANSPLANTATION, (1993 Sep) 56 (3) 633-8. Journal code: 0132144. ISSN: 0041-1337. Pub. country: United States. Language: English.

AB Diabetic (B6) (IE-) mice treated with a depleting regimen of anti-CD4 monoclonal antibody at the time of transplantation with A/J (IEK) islets of Langerhans showed indefinite acceptance of their islet allograft, as evidenced by persistent normoglycemia. To address the mechanisms involved in such anti-CD4 induced transplantation tolerance we studied potentially IE-reactive V beta 11+ T cells from the tolerant allografted mice. Following complete repopulation of the CD4+ cells, both the CD4+V beta 11+ and CD8+V beta 11+ T cell subsets of the transplanted mice were unresponsive to anti-V beta 11 specific crosslinking. In contrast, lymphocytes tested within the first ten days following transplant were responsive to anti-V beta 11 specific crosslinking; this response decreased as a function of time and reached background levels by day 120 posttransplant. Sorting experiments indicated that the response of lymphocytes to anti-V beta 11 specific crosslinking seen during the initial 120 days posttransplant was confined to the peripheral CD8+ cells; the repopulating CD4+V beta 11+ T cells were unresponsive. In addition, administration of r-IL-2 at the time of transplantation induced rejection in anti-CD4-treated animals, again indicating that the peripheral CD8+ cells could respond shortly after transplant if provided with appropriate help. The decreasing response of CD8+ T cells from transplanted animals to anti-V beta 11 stimulation was inversely correlated with the rate of migration of cells from the thymus to the periphery, implying that new thymic migrant V beta 11+ cells, both CD4+ and CD8+, were rendered anergic upon encountering peripheral alloantigen. These data suggest the possibility that recent thymic migrants are rendered anergic upon encountering antigen in the periphery, a simple model to serve as a "fail-safe" mechanism to prevent autoreactivity.

- L8 ANSWER 24 OF 30 MEDLINE DUPLICATE 8
 93127211 Document Number: 93127211. PubMed ID: 8420037. Evidence that anti-CD8 abrogates anti-CD4-mediated clonal **anergy** but allows allograft survival in mice. Song H K; Alters S E; **Fathman C G**. (Department of Medicine, Stanford University School of Medicine, California 94305-5111.) TRANSPLANTATION, (1993 Jan) 55 (1) 133-9. Journal code: 0132144. ISSN: 0041-1337. Pub. country: United States. Language: English.
- AB Monoclonal antibodies directed against different T cell subpopulations have been used in several rodent models of transplantation to induce long-term unresponsiveness to allografts by a variety of mechanisms. To investigate whether different mechanisms may be operative when different regimens of mAb therapy are used, we studied the effects of various combinations of anti-T-cell antibody treatment on the induction of tolerance in a mouse islet allograft model. Anti-CD4 mAb alone, anti-CD8 mAb alone, anti-CD4 mAb plus anti-CD8 mAb, and anti-Thy1.2 mAb alone were given at the time of engraftment. Only the anti-CD4 mAb and the anti-CD4 mAb plus anti-CD8 mAb regimens were successful in inducing permanent unresponsiveness to islet allografts. We have previously shown that anti-CD4 mAb alone induces permanent unresponsiveness to islet allografts by a mechanism of clonal **anergy**, as demonstrated by unresponsiveness of potentially alloreactive T cells to anti-T-cell receptor-specific cross-linking. Interestingly, the potentially alloreactive T cell subsets of recipient mice (V beta 5+ and V beta 11+) made unresponsive to islet allografts by anti-CD4 mAb plus anti-CD8 mAb therapy were not found to be anergic using the same assay. Differences between the repopulation kinetics of CD8+ T cells of anti-CD4 mAb plus anti-CD8 mAb treated recipient mice, which accepted islet allografts, and anti-Thy1.2 treated recipient mice, which rejected islet allografts despite similar levels of initial T cell depletion, suggest that unresponsiveness to alloantigen may have been induced in anti-CD4 mAb plus anti-CD8 mAb treated recipients by clearance of donor passenger leukocytes during prolonged CD8+ T cell depletion.
- L8 ANSWER 25 OF 30 MEDLINE DUPLICATE 9
 93117858 Document Number: 93117858. PubMed ID: 8418801. Requirement for CD8+ cells in T cell receptor peptide-induced clonal unresponsiveness. Gaur A; Ruberti G; Haspel R; Mayer J F; **Fathman C G**. (Department of Medicine, Stanford University School of Medicine, CA 94305.) SCIENCE, (1993 Jan 1) 259 (5091) 91-4. Journal code: 0040511. ISSN: 0036-8075. Pub. country: United States. Language: English.
- AB T cell receptor (TCR) vaccination in rats prevents the development of experimental allergic encephalomyelitis (EAE), an animal model of multiple sclerosis. The mechanism of this potential immunotherapy was examined by vaccinating mice with an immunogenic peptide fragment of the variable region of the TCR V beta 8.2 gene. Another immunogen that usually induces an immune response mediated by V beta 8.2+ T cells was subsequently inhibited because specific clonal unresponsiveness (**anergy**) had been induced. Depletion of CD8+ cells before TCR peptide vaccination blocked such inhibition. Thus, the clonal **anergy** was dependent on CD8+ T cells, and such immunoregulatory T cells may participate in the normal course of EAE.
- L8 ANSWER 26 OF 30 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 10
 1993:141685 Document No.: PREV199344114885. **Anergy** induced by synthetic peptides of myelin basic protein blocks progression of autoimmune encephalomyelitis. Gaur, Amitabh (1); Wiers, B. (1); Rothbard, J.; **Fathman, C. Garrison**. (1) Div. Immunol. Rheumatol., Dep. Med., Stanford Univ. Med. Cent., Stanford, CA 94305 USA. Journal of Cellular Biochemistry Supplement, (1993) Vol. 0, No. 17 PART C, pp. 68. Meeting Info.: Keystone Symposium on Emerging Principles for Vaccine

Development: Antigen Processing and Presentations Taos, New Mexico, USA
February 8-14, 1993 ISSN: 0732-1959. Language: English.

L8 ANSWER 17 OF 30 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE
11

1992:192861 Document No.: BR43:5211. CLONAL **ANERGY** INDUCED IN THYMIC
MIGRANT CELLS DURING ANTI-CD4 INDUCED TRANSPLANTATION TOLERANCE. ALTERS S
E; SONG H K; **FATHMAN C G**. DEP. MED./IMMUNOL., S-021, STANFORD
UNIV. SCH. MED., STANFORD, CALIF. 94305.. MEETING OF THE FEDERATION OF
AMERICAN SOCIETIES FOR EXPERIMENTAL BIOLOGY (FASEB) PART II, ANAHEIM,
CALIFORNIA, USA, APRIL 5-9, 1992. FASEB (FED AM SOC EXP BIOL) J. (1992) 6
(5), A1702. CODEN: FAJOC. ISSN: 0892-8638. Language: English.

L8 ANSWER 18 OF 30 MEDLINE DUPLICATE 12
93068334 Document Number: 93068334. PubMed ID: 1279812. Amelioration of
autoimmune encephalomyelitis by myelin basic protein synthetic
peptide-induced **anergy**. Gaur A; Wiers B; Liu A; Rothbard J;
Fathman C G. (Stanford University School of Medicine, Division of
Immunology and Rheumatology, CA 94305.) SCIENCE, (1992 Nov 27) 258 (5087)
1491-4. Journal code: 0404511. ISSN: 0036-8075. Pub. country: United
States. Language: English.

AB Experimental autoimmune encephalomyelitis (EAE), a demyelinating disease
of the central nervous system that can be induced in susceptible strains
of mice by immunization with myelin basic protein (MBP) or its
immunodominant T cell determinants, serves as a model of human multiple
sclerosis. Tolerance to MBP in adult mice was induced by intraperitoneal
injection of synthetic peptides of immunodominant determinants of MBP and
prevented MBP-induced EAE. Furthermore, tolerance-inducing regimens of
peptides administered to mice after the disease had begun (10 days after
induction with MBP) blocked the progression and decreased the severity of
EAE. Peptide-induced tolerance resulted from the induction of
anergy in proliferative, antigen-specific T cells.

L8 ANSWER 19 OF 30 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.DUPLICATE 13
92355607 EMBASE Document No.: 1992355607. Anti-CD4 monoclonal antibodies in
therapy: Creation of nonclassical tolerance in the adult. Shizuru J.A.;
Alters S.E.; **Fathman C.G.**. Stanford Univ. School of Medicine,
Div. of Rheumatology and Immunology, Stanford, CA 94305, United States.
Immunological Reviews -/129 (105-130) 1992.
ISSN: 0105-2896. CODEN: IMPEDL. Pub. Country: Denmark. Language: English.
Summary Language: English.

AB We have described the studies from our laboratory which demonstrate that
depleting anti-CD4 mAb induce tolerance to foreign antigens in adult,
euthymic animals. Further, we have proposed that such tolerance occurs as
a result of new thymic migrants encountering antigens in the periphery.
However, these conclusions can be considered only partial since we (Song
et al. in press) and others have shown that depletion of T cells per se
does not permit tolerance. For example, anti-Thy-1 or anti-Lyt-1 are
themselves immunosuppressive and able to deplete T cells, yet they elicit
strong anti-globulin responses against themselves and do not permit
tolerance to be induced either to transplants or administered soluble
protein antigen. We have recently found that while the combination of
anti-CD4 and anti-CD8 mAb allows long-term survival of allografted islets
in mice, **anergy** in the relevant T-cell subsets was not found (in
contrast to what is found with anti-CD4 mAb treatment alone) (Song et al.
in press). In this instance, long-term survival was probably the result of
changes in graft immunogeneity (i.e., migration of passenger leukocytes)
since the kinetics of repopulation were much delayed in the anti-CD4 and
-CD8 treated mice. As discussed elsewhere in this volume, interesting
studies from several laboratories suggest that non-depleting anti-CD4 mAb
can generate unresponsiveness in a variety of systems. In reviewing the
literature it is clear that the success of non-depleting reagents appears
to be dependent upon the model system tested. For example, although

depleting and nondepleting CD4 mAb regimens produced comparable prolongation of cultured fetal pancreas allografts in mice (Charlton and Mandel), almost total elimination of circulating CD4+ cells did not prevent acute rejection of murine skin grafts (Auchincloss et al. 1988). This heterogeneity is not surprising given the multiple functional roles of the CD4 molecule and the cells that bear this molecule. In addition to depletion, antibodies directed against CD4 can potentially affect CD4+ cell function by (1) direct blockade or failure to augment the formation of the TCR-antigen/MHC ternary complex or (2) by transmitting a negative signal to the CD4 T cell or interfering with normal signal transduction mechanisms. Undoubtedly, it is a combination of mechanisms that allows these antibodies their immunosuppressive effects. What can be said with certainty is that these antibodies will continue to be important tools for understanding the molecular and cellular basis of the immune response, and will soon emerge as invaluable therapeutic agents in the clinical arena.

L8 ANSWER 10 OF 30 MEDLINE DUPLICATE 14
 91108348 Document Number: 91108348. PubMed ID: 1899105. Anti-CD4 mediates clonal **anergy** during transplantation tolerance induction. Alters S E; Shizuru J A; Ackerman C; Grossman D; Seydel K B; Fathman C G . (Department of Medicine, Stanford University School of Medicine, California 94305.) JOURNAL OF EXPERIMENTAL MEDICINE, (1991 Feb 1) 173 (2) 491-4. Journal code: 2985109R. ISSN: 0022-1007. Pub. country: United States. Language: English.

AB Depletion of CD4+ cells using anti-CD4 monoclonal antibodies leads to allograft tolerance. Here we show that anti-CD4-mediated tolerance to pancreatic islets of Langerhans transplanted from an A/J (IEk) donor to a diabetic C57Bl/6 (B6) (IE-) recipient occurs in the absence of clonal deletion of the potentially IE-reactive V beta 11+ T cells. Instead, a state of clonal **anergy** is induced in both the CD4+V beta 11+ and CD8+V beta 11+ T cell subsets. This clonal **anergy** can be partially overcome in vitro by the addition of recombinant interleukin 2.

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FILE 'MEDLINE, EMBASE, BIOSIS, SCISEARCH, CAPLUS' ENTERED AT 08:24:54 ON 31 OCT 2002

L1 0 S "GRAIL PROTEIN"
 L2 1987 S GRAIL
 L3 181 S L2 AND PROTEIN
 L4 3 S L3 AND ANERGY
 L5 2 DUP REMOVE L4 (1 DUPLICATE REMOVED)
 L6 5313 S (FORD, G?/AU OR BLOOM D?/AU OR FATHMAN G?/AU OR FATHMAN C?/AU
 L7 29 S L6 AND ANERGY
 L8 30 DUP REMOVE L7 (39 DUPLICATES REMOVED)

=> s 18 and GRAIL

L9 2 L8 AND GRAIL

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PROCESSING COMPLETED FOR L9

L10 2 DUP REMOVE L9 (0 DUPLICATES REMOVED)

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L10 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2002 ACS

2001:933513 Document No. 135:370654 Human and mouse **anergy**

associated genes GRAIL. Ford, Gregory S.; Bloom,

Debra; Fathman, C. Garrison (The Board of Trustees of the

Leland Stanford Junior University, USA). PPT Int. Appl. WO 2001085943 A1

20011115, 50 pp. DESIGNATED STATES: W: AU, CA, JP; PW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR. (English). CODEN: PIMXD2. APPLICATION: WC 2001-US15385 20010511. PRIORITY: US 2000-PV-03513 20000511.

AB Isolated nucleic acid compns. and sequences of **anergy** associ. genes are provided, including the novel **GRAIL** gene. Expression of these genes is unregulated during the early stages of induction of **anergy**. The murine **GRAIL** sequence is shown to attenuate IL-2 transcription in T cells during response to antigenic stimulation. The identification of genes involved in the induction of **anergy** is useful in the evaluation of the pathophysiol. or immunotherapy of cancer, autoimmune disease, and transplant rejection. Genetic sequences involved in **anergy** induction are useful markers in the evaluation of specific immunotherapies. Functional characterization of genes involved in **anergy** induction allows the elucidation of the mechanism(s) of T cell **anergy**, including the transcriptional blockade of IL-2, which may be manipulated to regulate T cell responses in human disease. The signaling pathways involving **GRAIL** are of significant interest in the identification of drugs that either block or upregulate the function(s) of **GRAIL**.

L10 ANSWER 2 OF 2 MEDLINE

2001544740 Document Number: 21475847. PubMed ID: 11591749. CD4(+)CD25(+) T cells facilitate the induction of T cell **anergy**. Ermann J; Szanya V; Ford G S; Paragas V; Fathman C G; Lejon K. (Division of Immunology and Rheumatology, Department of Medicine, Stanford University School of Medicine, Stanford, CA 94305, USA.) JOURNAL OF IMMUNOLOGY, (2001 Oct 15) 167 (8) 4271-5. Journal code: 1985117R. ISSN: 0022-1767. Pub. country: United States. Language: English.

AB T cell **anergy** is characterized by the inability of the T cell to produce IL-2 and proliferate. It is reversible by the addition of exogenous IL-2. A similar state of unresponsiveness is observed when the proliferative response of murine CD4(+)CD25(-) T cells is suppressed in vitro by coactivated CD4(+)CD25(+) T cells. We have developed a suppression system that uses beads coated with anti-CD3 and anti-CD28 Abs as surrogate APCs to study the interaction of CD4(+)CD25(+) and CD4(+)CD25(-) T cells in vitro. CD4(+)CD25(+) T cell-induced suppression, in this model, was not abrogated by blocking the B7-CTLA-4 pathway. When the CD4(+)CD25(-) T cells were separated from the CD4(+)CD25(+) suppressor cells after 24 h of coactivation by the Ab-coated beads, the CD4(+)CD25(-) T cells were unable to proliferate or to produce IL-2 upon restimulation. The induction of this anergic phenotype in the CD4(+)CD25(-) T cells correlated with the up-regulated expression of the gene related to **anergy** in lymphocytes (**GRAIL**), a novel **anergy**-related gene that acts as a negative regulator of IL-2 transcription. This system constitutes a novel mechanism of **anergy** induction in the presence of costimulation.

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=> LOG Y

COST IN U.S. DOLLARS

SINCE FILE
ENTRY

TOTAL
SESSION

FULL ESTIMATED COST	89.53	89.74
DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE	TOTAL
	ENTRY	SESSION
CA SUBSCRIBER PRICE	-2.48	-2.48

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OM nucleic - nucleic search, using sw model

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Title: US-09-854-300-7

Perfect score: 1774

Sequence: 1 actgagagctccacgcgggt.....ataggagagttctctctcag 1774

Scoring table: IDENTITY_NUC

Gapop 10 0 0 Gapext 1 0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109290

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.par.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
- 27: em.sts.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htg_hum.*
- 31: em.htg_inv.*
- 32: em.htg_other.*
- 33: em.htg_mus.*
- 34: em.htg_pln.*
- 35: em.htg_rtd.*
- 36: em.htg_vrt.*
- 37: em.htg_vrt.*
- 38: em.sy.*
- 39: em.htgo_hum.*
- 40: em.htgo_mus.*
- 41: em.htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1662.8	93.7	2796	6	AX337968 Sequence
2	1650.6	93.6	2810	9	AK074264 Homo sapi
3	1280.8	72.2	1297	9	AF394689 Homo sapi
4	1205.2	67.9	1938	10	BC010477 Mus muscu
5	1203.6	67.8	1936	10	AB041548 Mus muscu
6	1106.8	62.3	1287	10	AF428411 Mus muscu
7	714.4	40.3	1871	9	AK027169 Homo sapi
8	674.4	38.0	169812	9	AL391315 Human DNA
9	674.4	38.0	169863	2	AL591467 Homo sapi
10	392.2	22.1	404	6	AK071980 Sequence
11	372.6	21.0	646	6	AX341568 Sequence
12	331.0	17.5	435	6	AX396961 Sequence
13	290.4	15.8	195263	2	AC115936 Mus muscu
14	278.4	15.7	167021	2	AC111461 Rattus no
15	268.8	15.2	1391	9	AB070023 Macaca fa
16	268.8	15.2	1395	9	AB070058 Macaca fa
17	266.8	15.0	1429	9	AK098524 Homo sapi
18	266.8	15.0	1430	9	BC022038 Homo sapi
19	266.8	15.0	1446	9	AF447589 Homo sapi
20	266.8	15.0	120984	9	AC006463 Homo sapi
21	256.4	14.5	1328	9	BC029264 Homo sapi
22	254.8	14.4	1355	6	AK061659 Sequence
23	253.2	14.3	1261	9	AK098654 Homo sapi
24	220.2	12.4	116739	2	AC114183 Rattus no
25	220.2	12.4	140345	2	AC109686 Rattus no
26	217.4	12.3	116739	10	AL731648 Mouse DNA
27	217.4	12.3	116739	2	AC114183 Rattus no
28	209	11.8	1200	6	AK083416 Sequence
29	209	11.8	1547	6	AX083425 Sequence
30	209	11.8	2001	9	BC019355 Homo sapi
31	207.4	11.7	2013	9	BC032328 Homo sapi
32	156.8	8.8	839	9	AK058116 Homo sapi
33	148.8	8.4	1452	10	AF171875 Homo sapi
34	148.8	8.4	1506	10	BC018199 Mus muscu
35	147.6	8.3	1153	9	AF155650 Human mRN
36	147.6	8.3	1253	6	AK030960 Sequence
37	147.6	8.3	1257	6	AK083320 Sequence
38	147.6	8.3	1433	6	AX083330 Sequence
39	147.6	8.3	1445	9	BC017100 Homo sapi
40	140	7.9	118766	2	AC128696 Rattus no
41	108.4	6.1	5111	9	AB033040 Homo sapi
42	105.6	6.0	382	6	AX261677 Sequence
43	87.2	4.9	2369	3	DROGOLTHA M97204 Fruitfly go
44	84.8	4.8	2586	3	AY069169 Drosophil
45	79	4.5	2449	4	AJ132110 Cryptoblag

ALIGNMENTS

RESULT 1	AX337968	AX337968	2796 bp	DNA	linear	PAT 09-JAN-2002
LOCUS	Sequence	9 from Patent WO0194391.				
DEFINITION	AX337968					
ACCESSION	AX337968					
VERSION	AX337968.1	GI:18128679				
KEYWORDS	human.					
SOURCE	Homo sapiens					
ORGANISM	Fukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1					
AUTHORS	Yue H., He A., Nguyen D.B., Yao M.G., Bandman O., Burford N., Tang Y.T., Xu Y., Hafalia A., Azimzai Y. and Wallis N.K.					
TITLE	Intracellular signaling proteins					

AL591467.3	GI:14348539
HTG:	HTGS_PHASE; HTGS_CANCELLED.
SOURCE	human.
ORGANISM	Homo sapiens
Eukaryota;	Metazoa;
Mammalia;	Eutheria;
Primates;	Catarrhini;
Hominidae;	Homo.
Bird.C.	(bases 1 to 169863)
REFERENCE	
AUTHORS	Direct Submission
JOURNAL	Submitted (10-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk requests: clonerequest@sanger.ac.uk On Jun 12, 2001 this sequence version replaced gi.14268300. ----- Genome Center Center: Sanger Centre
COMMENT	Center code: SC Web site: http://www.sanger.ac.uk Contact: humquery@sanger.ac.uk ----- Project Information Center project name: BA697G3 ----- Summary Statistics Assembly program: XGAP4; version: 4.5 Sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 157318 bases at least Q40 Consensus quality: 157886 bases at least Q30 Consensus quality: 158243 bases at least Q20 Insert size: 169863; sum-of-contigs Insert size: 169949; 0.8% error; agarose-fp Quality coverage: 5.85x in Q20 bases, sum-of-contigs Quality coverage: 6.91x in Q20 bases; agarose-fp ----- * NOTE: This is a 'working draft' sequence. * This sequence will be replaced * by the finished sequence as soon as it is available and * the accession number will be preserved.
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	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/chromosome="X"
	/clone="RP11-697G3"
	/clone_lib="RPC1-11.3"
misc_feature	1..169863
	/note="assembly_fragment:02868"
BASE COUNT	51891 a 31100 c 31417 g 55455 t
ORIGIN	
Query Match	38.0%; Score 674.4; DB 2; Length 169863;
Best Local Similarity	99.9%; Pred.No. 1.9e+143;
Matches 675;	Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Dy	CGAGAGACCTATTTTGGGCAAAATTGTGGTGTCGAACACTAAGTAAGTCCGTCGTCGCAGC 144
Dd	CGGAGGACCTCATCTGGGCAAAATTGTGGTGTCGAACACTAAGTAAGTCCGTCGTCGCAGC 23968
Qy	TAGCTGGCAGCTCCCATCTCTCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 193
Dd	TAGCTGGCAGCTCCCATCTCTCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 23968
Qy	ACCAGGCTCTGCCAAGGGCTAGGAGGGGCGTGGCGAGGGGCGGTAGGTAAGTCGGGAGG 253
Dd	ACCAGGCTCTGCCAAGGGCTAGGAGGGGCGTGGCGAGGGGCGGTAGGTAAGTCGGGAGG 24068
Qy	GCGCGGCTATGCGGCG 414
Dd	GCGCGGCTATGCGGCG 24144
Qy	TCCAGATTCGCTGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 424
Dd	TCCAGATTCGCTGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 24208
Y	GSSGCTGAAGTAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAG 433


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QY 1434 TAAACATTAAGTAAATTTCTGTCAGTGTGATGTTATTCCTGATATGAGCAAAATTAAT 1433
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DB 247 TAAACATTAAGTAAATTTCTGTCAGTGTGATGTTATTCCTGATATGAGCAAAATTAAT 406
|||||

QY 1494 TTGAAGACGAGAACTGCTTAATCAAGAGACTGCTGTTCGAGAAATTAATCTTAAATC 1553
|||||
DB 307 TTGAAGACGAGAACTGCTTAATCAAGAGACTGCTGTTCGAGAAATTAATCTTAAATC 406
|||||

QY 1554 TGTGTAATAGAAACTTGAACCATTTAGTAATAACAGA 1591
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DB 367 TGTGTAATAGAAACTTGAACCATTTAGTAATAACAGA 404
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RESULT 11
AX341568
LOCUS AX341568 646 bp DNA linear PAT 10-JAN-2002
DEFINITION Sequence 1815 from Patent WO0196388.
ACCESSION AX341568
VERSION AX341568.1 GI:18137550
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Jiang, Y., Harlocker, S.L. and Secrist, H.
TITLE Compositions and methods for the therapy and diagnosis of colon
cancer
JOURNAL Patent: WO 0196388-A 1815 20-DEC-2001;
CORIXA CORPORATION (US)
FEATURES
Source 1. 646
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 226 a 103 c 106 g 208 t 3 others
ORIGIN
Query Match 21.0%; Score 372.6; DB 6; Length 646;
Best Local Similarity 98.0%; Pred. No. 9.7e-75;
Matches 398; Conservative 0; Mismatches 5; Indels 3; Gaps 2;

QY 1369 ACAGGAAATAGATGAACCGCCCTCTGGAGCAACACCTGTCATCAACAATGAAAGCTTACA 1428
|||||
DB 1 ACAGGAAATAGATGAACCGCCCTCTGGAGCAACACCTGTCATCAACAATGAAAGCTTACA 60
|||||

QY 1429 GTGTGTAATCAAGTAAATTTCTGTCAGTGTGATGTTATTCCTGATATGAGCAAAATTA 1488
|||||
DB 61 GTGTGTAATCAAGTAAATTTCTGTCAGTGTGATGTTATTCCTGATATGAGCAAAATTA 129
|||||

QY 1489 AACCTTTGAAGAGAGCAAACTGCTTAATCAAGAGACTGCTGTTCGAGAAATTAATCTTAA 1548
|||||
DB 121 AACCTTTGAAGAGAGCAAACTGCTTAATCAAGAGACTGCTGTTCGAGAAATTAATCTTAA 180
|||||

QY 1549 AAATCTCTGTAATTAAGAAATTTGAAGCAATTAAGTAAATTAAGTAAATTAAGTAAATTA 1608
|||||
DB 181 AAATCTCTGTAATTAAGAAATTTGAAGCAATTAAGTAAATTAAGTAAATTAAGTAAATTA 240
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QY 1609 AGTTCTTATTAATTAATTTGATAAAATTTAATAAATAGAGTGTGATGTTAAAGTGTCTAG 1668
|||||
DB 241 AGTTCTTATTAATTAATTTGATAAAATTTAATAAATAGAGTGTGATGTTAAAGTGTCTAG 400
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QY 1669 ATGACTAATATTGCTATAGTTAAATGGCTTAAATATTAATTTACCTGTTAACTTTT 1728
|||||
DB 301 ATGACTAATATTGCTATAGTTAAATGGCTTAAATATTAATTTACCTGTTAACTTTT 358
|||||

QY 1729 CCACCAACTCATTATAATATTTTTCATAGGCAAGTTTCCCTCTCAG 1774
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DB 359 CCA-CAAACTCATTATAATATTTTTCATAGGCAAGTTTCCCTCTCAG 403
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RESULT 12
AX396961/c

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LOCUS AX396961 435 bp DNA linear PAT 18-MAY-2002
DEFINITION Sequence 1176 from Patent WO0212328.
ACCESSION AX396961
VERSION AX396961.1 GI:21067708
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS King, G.E., Meagher, M.J., Xu, J. and Secrist, H.
TITLE Compositions and methods for the therapy and diagnosis of colon
cancer
JOURNAL Patent: WO 0212328-A 1176 14-FEB-2002;
CORIXA CORPORATION (US)
FEATURES
Source 1. 435
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 147 a 62 c 69 g 157 t
ORIGIN
Query Match 17.5%; Score 310; DB 6; Length 435;
Best Local Similarity 97.4%; Pred. No. 2e-60;
Matches 336; Conservative 0; Mismatches 6; Indels 3; Gaps 2;

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DB 435 CTGGTAAACCATGAAGCAAAATTTCTGGCAGTGGATGTTATTCCTCATGNGCAACCCA 376
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QY 1490 ACCTTTGAAGAGAGCAAACTGCTTAATCAAGAGACTGCTGTTCGAGAAATTAATCTTAA 1549
|||||
DB 375 ACCTTTGAAGAGAGCAAACTGCTTAATCAAGAGACTGCTGTTCGAGAAATTAATCTTAA 316
|||||

QY 1550 ATCTGCTGTATATAGAAAATTTGACCATTTAGTAATACAGAACTGCAATCAGGGGCTA 1609
|||||
DB 315 ATCTGCTGTATATAGAAAATTTGACCATTTAGTAATACAGAACTGCAATCAGGGGCTA 256
|||||

QY 1610 GTTCTATTATTAATTTGATATAATTTTAAATAAGAGAGTACTACTGAAAGTGTCTCAG 1669
|||||
DB 255 GTTCTATTATTAATTTGATATAATTTTAAATAAGAGTACTACTGAAAGTGTCTCAG 196
|||||

QY 1670 TGACTAATATTATGCTATAGTTAAATGGCTTAAATATTAATTAATTTTAACTGTTAACTTTTTC 1729
|||||
DB 195 TGACTAATATTATGCTATAGTTAAATGGCTTAAATATTAATTAATTTTAACTGTTAACTTTTTC 138
|||||

QY 1730 CACCAAACTCATTATAATATTTTTCATAGGCAAGTTTCCCTCTCAG 1774
|||||
DB 137 CCA-CAAACTCATTATAATATTTTTCATAGGCAAGTTTCCCTCTCAG 94
|||||

RESULT 13
AX115936/c
LOCUS AX115936 195263 bp DNA linear HTG 20-JUN-2002
DEFINITION Mus musculus clone PP24-545D3, WORKING DRAFT SEQUENCE, 13 ordered
pieces.
ACCESSION AX115936
VERSION AX115936.3 GI:21490425
KEYWORDS HTG: HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 195263)
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L.,
Boukhalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
Cook, A., Cooke, P., DeArelano, K., Dewar, K., Diaz, J. S., Dodge, S.,

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* consists of 75 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1200: contig of 1200 bp in length
* 1301: gap of unknown length
* 1301: contig of 1180 bp in length
* 2481: gap of unknown length
* 2581: contig of 1714 bp in length
* 4295: gap of unknown length
* 4395: contig of 1195 bp in length
* 5590: gap of unknown length
* 5690: contig of 1350 bp in length
* 7040: gap of unknown length
* 7140: contig of 1022 bp in length
* 8162: gap of unknown length
* 8262: contig of 1525 bp in length
* 9787: gap of unknown length
* 9887: contig of 1189 bp in length
* 11076: gap of unknown length
* 11176: contig of 1312 bp in length
* 12488: gap of unknown length
* 12588: contig of 1152 bp in length
* 13740: gap of unknown length
* 13840: contig of 1265 bp in length
* 15105: gap of unknown length
* 15205: contig of 1402 bp in length
* 16607: gap of unknown length
* 16707: contig of 1391 bp in length
* 18098: gap of unknown length
* 18197: contig of 1569 bp in length
* 19767: gap of unknown length
* 19867: contig of 1869 bp in length
* 21736: gap of unknown length
* 21836: contig of 1036 bp in length
* 22872: gap of unknown length
* 22972: contig of 1089 bp in length
* 24061: gap of unknown length
* 24160: contig of 1419 bp in length
* 25579: gap of unknown length
* 25679: contig of 1467 bp in length
* 25680: gap of unknown length
* 27147: contig of 1542 bp in length
* 27246: gap of unknown length
* 27247: contig of 1142 bp in length
* 28388: gap of unknown length
* 28489: contig of 1585 bp in length
* 30074: gap of unknown length
* 30174: contig of 1234 bp in length
* 31408: gap of unknown length
* 31507: contig of 1542 bp in length
* 31508: gap of unknown length
* 33049: contig of 1707 bp in length
* 33149: gap of unknown length
* 33150: contig of 1247 bp in length
* 34856: gap of unknown length
* 34957: contig of 1723 bp in length
* 36203: gap of unknown length
* 36304: contig of 1005 bp in length
* 38027: gap of unknown length
* 38127: contig of 1650 bp in length
* 39132: gap of unknown length
* 39231: contig of 1650 bp in length
* 40881: gap of unknown length
* 40981: contig of 1241 bp in length
* 42223: gap of unknown length
* 42323: contig of 1657 bp in length
* 42323: gap of unknown length
* 43980: contig of 1627 bp in length
* 44080: gap of unknown length
* 45707: contig of 1657 bp in length
* 47463: gap of unknown length
* 47563: contig of 1507 bp in length
* 47564: gap of unknown length
* 49071: contig of 1507 bp in length
* 49170: gap of unknown length

* 49171: contig of 1724 bp in length
* 50894: gap of unknown length
* 50895: contig of 1493 bp in length
* 52487: gap of unknown length
* 52488: contig of 2293 bp in length
* 54881: gap of unknown length
* 54881: contig of 2393 bp in length
* 57373: gap of unknown length
* 57374: contig of 1018 bp in length
* 58491: gap of unknown length
* 58492: contig of 1292 bp in length
* 59883: gap of unknown length
* 59884: contig of 1381 bp in length
* 61364: gap of unknown length
* 61464: contig of 1336 bp in length
* 62800: gap of unknown length
* 62801: contig of 1501 bp in length
* 64401: gap of unknown length
* 64501: contig of 2325 bp in length
* 66826: gap of unknown length
* 66927: contig of 1009 bp in length
* 67935: gap of unknown length
* 68035: contig of 2477 bp in length
* 70512: gap of unknown length
* 70513: contig of 1985 bp in length
* 72597: gap of unknown length
* 72697: contig of 1782 bp in length
* 74479: gap of unknown length
* 74480: contig of 2251 bp in length
* 74580: gap of unknown length
* 76831: contig of 2868 bp in length
* 76931: gap of unknown length
* 79799: gap of unknown length
* 79898: contig of 2756 bp in length
* 82654: gap of unknown length
* 82655: contig of 1931 bp in length
* 84685: gap of unknown length
* 84686: contig of 2634 bp in length
* 84786: gap of unknown length
* 87420: contig of 4472 bp in length
* 87520: gap of unknown length
* 89991: gap of unknown length
* 90091: contig of 1736 bp in length
* 90092: gap of unknown length

Query Match 15.7% Score 278.4; DB 2: Length 167021;
Best Local Similarity 60.7%; Pred. No. 1.3e-52;
Matches 544; Conservative 0; Mismatches 316; Indels 36; Gaps 4;

QY 434 GTGAACCGTAGCGGTGGGAGCTGAGCGAGGAGGGCGGTGTACGCCAGGACTCGCGCTG 493
DB 83860 GGGAAACGATGCTGAGAGCTGGGAGAGACTGGGGTCTTCGGAAGAACTCCATCTTG 83801
QY 494 GAGCGCTGTGGGTGCTTGTGTACCGTCTTCACGCGCGCGGGGCTTAAAGCGCTCTAAC 553
DB 83800 AAGACAGTANTAGGANTANTTTGTGCCACAGAGGAGAA---AATTCAAAATGTTGAC 83744
QY 554 CGGCACAGGAATTTACGGTGGCCACCGGTTTGGGAGAGCACCGGCAAGTCTTTGGTTG 613
DB 83743 GCGAATACAGTTCATCTGTGTGCGGAA-----CAAGAGCGGTGGATT 83699
QY 614 GCGCTCATCTAACTGCGGCGGCGGCTTACCTTGGACACAGATCGCATCGGCTTATGAG 673
DB 83698 GCACTCATGAA---AGGGAGGTTTGGCCCTTCACAGAAATCAAAATGGCATCTGAG 83642
QY 674 AGATGGGCGTCTGGAGCGGCTCATCTTTAACTTCCCGGGGACCGCGCAATGAGTCTATCCCG 733
DB 83641 AATGGGCGCGGCGGAGTGATCATATACTTTCCGCGGAGTCTGCAACAGGTTTTCGCC 83582
QY 734 ATGTCTCACCGCGGTCGAGTAGACATGTTGCAATCATGATCGGCAATCTGAAGGCACA 793
DB 83581 ATGTCTCACCGAGCGTTTGAAGACATGTTGTATGATGATGTTGATGATGATGATGATG 83522
QY 794 AAAATCTGCAATCTATTCAAAGAGGCATACAGTACATGATGATGATGATGATGATGATG 853
DB 83521 GAGATTTTGCATTTAATTAGGAAGGAGTCCATGTTACCGTCTATGTTAGGTTGCGAGCA 83462

QY 1230 AAGCTTTGGGATTGAGTGGATCTTGAAGATGGAATCAATCTCTTTACAAAGTCCCTCTAT 1289
 DB 1102 AAGTTTGGGGATTCAAGTGGATCTTGAAGATGGAAGAACCTTTGCAAGTCTTAATGT 1161
 QY 1290 CCAATGAATATCTAATAGTGGCTCCCTCCCATGAAGAGGATAATTCGACGGA 1341
 DB 1162 CAATGGAACCTGTCTCAAACTTATCATCTAATGAAGAGGAGACAAATACGA 1213

Search completed: October 31, 2002, 09:55:13
 Job time : 4991 secs

GenCore version 5.1.3

Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 31, 2002, 08:26:01 : Search time 2289 seconds

(without alignments)

12561 679 Million cell updates/sec

Title: US-09-854-300-7

Perfect score: 1774

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Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs. 809774376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

1: em_estba.*
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 3: em_estin.*
 4: em_estma.*
 5: em_estov.*
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 9: gb_est1.*
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 25: em_gss_other.*
 26: em_gss_pro.*
 27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1205.2	67.9	1921	AK018582	AK018582 Mus muscu
2	1202	67.8	2741	AK004847	AK004847 Mus muscu
3	836.8	47.2	1954	BC030951	BC030951 Homo sapi
4	680.4	38.4	1806	BC012931	BC012931 Homo sapi
5	673.8	38.0	811	B1600046	B1600046 603251431
6	654.2	36.9	1000	B1600419	B1600419 604244459

7	644.2	36.3	676	10	AV690200	AV690200
8	641	36.1	773	13	B1601096	B1601096
9	623.4	35.1	840	11	AK008312	Mus muscu
10	622.8	35.1	1150	13	B1488609	B1488609
11	622.4	35.1	906	12	BG165370	603246005
12	622.2	35.1	683	10	AV686169	AV686169
13	615.4	34.7	986	12	BG176206	BG176206
14	577	32.5	681	13	B1220592	603936079
15	564.4	31.8	683	10	AV692456	AV692456
16	542.8	30.6	557	13	BM507037	1h4405.Y
17	537.2	30.3	904	12	BF664617	602117901
18	531.2	29.9	596	12	BF231341	253699.BA
19	524.2	29.5	862	12	BF668554	602123601
20	515.6	29.1	902	12	BF665006	602344868
21	513.8	29.0	841	12	BF663559	602124911
22	509.8	28.7	812	13	B1110345	603900777
23	502.2	28.3	872	12	BF699229	603126878
24	499.4	28.2	789	12	BF669635	602120364
25	496	28.0	870	12	BF666897	603121530
26	492.4	27.8	759	12	BG400279	602464672
27	482.4	27.2	774	12	BG432146	602496225
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30	475.6	26.8	804	13	B1653069	603300779
31	471.8	26.6	856	12	BE958087	601644929
32	469	26.4	680	10	BE308209	601095109
33	468.6	26.4	884	12	BF542034	602069189
34	466.4	26.3	835	12	BE958350	601644838
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36	459.2	25.9	725	13	B1557834	603236825
37	458.6	25.9	466	12	BF382058	601816390
38	456.4	25.7	732	12	BF246687	601855477
39	443.6	25.0	813	13	B1648028	603279210
40	442.6	24.9	619	13	BG991456	602128561
41	441.8	24.9	889	12	BG172246	602333390
42	440	24.8	862	12	BF700761	602128561
43	435.4	24.5	854	12	BF670202	603124352
44	431.4	24.3	759	12	BE958295	601645073
45	427.2	24.1	942	12	BF967109	602287635

ALIGNMENTS

RESULT 1	AK018582	1921 bp	mRNA	linear	HFC 19-JAN-2002
LOCUS	Mus musculus adult male cecum cDNA, RIKEN full-length enriched library, clone:9130001F19:BRAIN CDNA, CLONE MNCB-3816, SIMILAR TO AF171875 G1-RELATED ZINC FINGER PROTEIN (MUS MUSCULUS), full insert sequence.				
ACCESSION	AK018582				
VERSION	AK018582.1	GI:12858361			
KEYWORDS	HTC: CAP trapper.				
SOURCE	Mus musculus (strain:G57BL/6J) adult male cecum cDNA to mRNA, clone.lib:RIKEN full-length enriched mouse cDNA library				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
AUTHORS	1 Carninci,P. and Hayashizaki,Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
MEDLINE	99279253				
PUBMED	10349636				
REFERENCE	2				
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
MEDLINE	20499274				

QY	732	CCATGCTCCACCCGGTGCAGTAGACATTGTTGCAATCATGATCGGCAATCTGAAAGCA	791	AK004847	2741 bp	mRNA	linear	HTC 19-JAN-2002
Db	658	CCATGCTCCACCCGGTGCAGTAGACATTGTTGCAATCATGATCGGCAATCTGAAAGCA	717	AK004847	2741 bp	mRNA	linear	HTC 19-JAN-2002
QY	792	CAAAAATTCGAAATCTATTCAAGAGGCATACAGTGCACAAATGTCATGAAAGTAGGGA	851	AK004847	2741 bp	mRNA	linear	HTC 19-JAN-2002
Db	718	CAAAAATTCGAAATCTATTCAAGAGGCATACAGTGCACAAATGTCATGAAAGTAGGGA	777	AK004847	2741 bp	mRNA	linear	HTC 19-JAN-2002
QY	852	AAAAACATGGCCCTGCGTGAATCAATTAATTTTCTGTTTCTGTTTCTGTTTCTGTTT	911	AK004847	2741 bp	mRNA	linear	HTC 19-JAN-2002
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QY	912	TTATTACGGCGCGCACTGCGGCTATTATTTATCTGCTGCAAGGCTACGGAATG	971	AK004847	2741 bp	mRNA	linear	HTC 19-JAN-2002
Db	838	TAATTACGGCGCGCACTGCGGCTATTATTTATCTGCTGCAAGGCTACGGAATG	897	AK004847	2741 bp	mRNA	linear	HTC 19-JAN-2002
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Db	898	CAAGAGCTCAAGAGGAGGAGGAGGCAATTAAGGCGAGATGCTTAAAGAACTATTGGAA	957	AK004847	2741 bp	mRNA	linear	HTC 19-JAN-2002
QY	1032	GGCTTCACTACGCACTGAAACAGGAGGAGGCAATTAAGGCGAGATGCTTAAAGAACT	1091	AK004847	2741 bp	mRNA	linear	HTC 19-JAN-2002
Db	958	GGCTTCACTACGCACTGAAACAGGAGGAGGCAATTAAGGCGAGATGCTTAAAGAACT	1017	AK004847	2741 bp	mRNA	linear	HTC 19-JAN-2002
QY	1092	GCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1151	AK004847	2741 bp	mRNA	linear	HTC 19-JAN-2002
Db	1018	GCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1077	AK004847	2741 bp	mRNA	linear	HTC 19-JAN-2002
QY	1152	ATATTTTCTAAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1211	AK004847	2741 bp	mRNA	linear	HTC 19-JAN-2002
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QY	1392	TGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1451	AK004847	2741 bp	mRNA	linear	HTC 19-JAN-2002
Db	1318	TGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1377	AK004847	2741 bp	mRNA	linear	HTC 19-JAN-2002
QY	1452	CTGTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1511	AK004847	2741 bp	mRNA	linear	HTC 19-JAN-2002
Db	1378	CTGTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1437	AK004847	2741 bp	mRNA	linear	HTC 19-JAN-2002
QY	1512	CTAATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1570	AK004847	2741 bp	mRNA	linear	HTC 19-JAN-2002
Db	1438	CTAATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1497	AK004847	2741 bp	mRNA	linear	HTC 19-JAN-2002
QY	1571	TAATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1628	AK004847	2741 bp	mRNA	linear	HTC 19-JAN-2002
Db	1498	TAATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1557	AK004847	2741 bp	mRNA	linear	HTC 19-JAN-2002
QY	1629	ATAAATTTAATAATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1688	AK004847	2741 bp	mRNA	linear	HTC 19-JAN-2002
Db	1558	ATAAATTTAATAATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1614	AK004847	2741 bp	mRNA	linear	HTC 19-JAN-2002
QY	1689	GTAAATGGCTTAAATATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAAT	1748	AK004847	2741 bp	mRNA	linear	HTC 19-JAN-2002
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QY	1749	TTTTTCATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1771	AK004847	2741 bp	mRNA	linear	HTC 19-JAN-2002
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AK004847 2741 bp mRNA linear HTC 19-JAN-2002
Mus musculus adult male liver cDNA, RIKEN full-length enriched library, clone:1300002C13:BRAIN CDNA, CLONE MNCB-3816, SIMILAR TO AF171875 G1-RELATED ZINC FINGER PROTEIN (MUS MUSCULUS), full insert sequence.
AK004847
AF004847.1 GI:12836339
HTC; CAP trapper.
Mus musculus (strain:G57BL/6J) adult male liver cDNA to mpna, clone.lib:RIKEN full-length enriched mouse cDNA library
clone:1300002C13.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.
1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159
3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, M., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, P., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohata, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
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4
Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, P., Kadota, Y., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staehli, P., Suzuki, P., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, P., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ping, B., Pingwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Teyo-oka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, I., Wynshaw-Boris, A., Yoshida, K., Hasedawa, Y., Kawai, H., Kohlsuki, S. and Hayashizaki, Y.
Functional annotation of a full-length mouse cDNA collection
Nature 406 (6821), 685-690 (2001)
21085660
11217851
5 (bases 1 to 2741)
Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, P., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T.,

QY 1392 TGGAGGAACACGTCGAGTCAACAAGTGAAGTCTCAGCTGCTAAACCATGAAGCAAAATT 1451
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BC030951 1054 bp mpNA linear HTC 13-JUN-2002
 LOCUS Homo sapiens, hypothetical protein FLJ23516, clone IMAGE:4280352,
 DEFINITION mRNA.
 ACCESSION BC030951
 VERSION BC030951.1 GI:21410659
 KEYWORDS HTC.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1954)
 Strausberg,R.
 Direct Submission
 Submitted (03-JUN-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgaps@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) mdj@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
 P. M.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 41 Row: C Column: 16
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 13375646
 This clone has the following problem: frame shifted.

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RESULT 4

BC012931
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 IMAGE:4456033, mRNA.
 ACCESSION BC012931
 VERSION BC012931.1 GI:15277870
 KEYWORDS HTC
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1806)
 Strausberg, R.
 Direct Submission
 Submitted (20-AUG-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabbs-re@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome
 Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: villalob@bcm.tmc.edu
 Villalob, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
 A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,
 Muzny, D.M., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAC Plate: 28 Row: b Column: 9
 This clone was selected for full length sequencing because it
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 This clone has the following problem: incomplete processing.

FEATURES

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 Db 481 ATTAATCTTAATATCTGTGAATAGAAACTTGAACCATAGTAATCAAGAGACTGCTG 540
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 QY 1598 AATCAGGGCTAGTCTTCTATTAAATTTGATAAATTTAATAAATGAAGAGTGTACTG 1657
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 Db 541 AATCAGGGCTAGTCTTCTATTAAATTTGATAAATTTAATAAATGAAGAGTGTACTG 600
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 QY 1658 AAGTCTCAGTACACTAATATATCTATAGTTAAATGGCTTAAATATTTAACTG 1717
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 Db 659 TTAACCTTTTCCCA-CAAACTCATTAATATATTTTCATAGCAAGTTTCCTCTCAG 714

RESULT 5
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 DEFINITION G3321431F1 NIH_MGC_26 Homo sapiens cDNA clone IMAGE:5303239 5';
 mRNA sequence.

ACCESSION BI600046
 VERSION BI600046.1 GI:15492985
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 811)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-re@mail.nih.gov

Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM11767 Row: n Column: 08
 High quality sequence stop: 776.

FEATURES

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/note="Organ: brain; Vector: pBluescriptP (modified
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 size-selected for average insert size 2.3 kb and
 normalized to ROT 5. This is a primary library enriched


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Db 380 GTGAACCGTACGGTGTGGAGCTGAGCGAGGAGGGCGTGTACGCCAGGACTCGCCGCTG 439
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Db 440 GAGCCTGTGGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 499
QY 554 CGGCACCAAAATTTTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 612
Db 500 CGGCACCAAAATTTTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 559
QY 613 GGCCTTCATCCAAACCGCGGGGGGCTGC-ACCTTCGGAGACAAATCATCTGCTGCTGCTGCTG 671
Db 560 GGCCTTCATCCAAACCGCGGGGGGCTGC-ACCTTCGGAGACAAATCATCTGCTGCTGCTGCTG 619
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LOCUS AV690200.1 GI:10292063
DEFINITION Homo sapiens cDNA clone pKCAR02 5', mRNA sequence.
ACCESSION AV690200
VERSION AV690200.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 674)
AUTHORS Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W.,
Shen, K., Lu, G., Fu, G., Cheng, M., Xu, S., Gu, W., Huang, W., Zhao, X.,
Hu, G., Gu, J., Chen, Z., and Han, Z.
TITLE Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26): 15089-15094 (2001)
MEDLINE 21625106
COMMENT Contact: Zequan Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzq@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
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/clone_lib="GKC"
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/dev_stage="Adult"
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XhoI"

BASE COUNT 94 a 223 c 231 g 125 t 3 others
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Matches 661; Conservative 0; Mismatches 11; Indels 2; Gaps 1;

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Db 64 TAGCTCGGAGCTGCCAGCTCCTCAGCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTC 123
QY 194 ACGAGGAGCTGCATCTCGCGCAACCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 253
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QY 254 GCGGAGGAGCTGCATCTCGCGCAACCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 313
Db 184 GCGGAGGAGCTGCATCTCGCGCAACCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 243
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Db 244 TCCAGATGCTGCCAGCTCCTCAGCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTG 303
QY 374 GCGGAGGAGCTGCATCTCGCGCAACCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 433
Db 304 GCGGAGGAGCTGCATCTCGCGCAACCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 363
QY 434 GTGAACCGTACGGTGTGGAGCTGAGCGAGGAGGGCGTGTACGCCAGGACTCGCCGCTG 493
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Db 484 CCGCACCAAAATTTTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 543
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QY 674 AGAGATGGCGCTGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 733
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DEFINITION Homo sapiens cDNA clone pKCAR02 5', mRNA sequence.
ACCESSION AV690200
VERSION AV690200.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 773)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

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cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLAM11762 row: p column: 21
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 BASE COUNT 130 a 242 c 254 g 146 t
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 LOCUS
 DEFINITION
 AK008312 840 bp mRNA linear HTC 19-JAN-2002
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 SIMILAR TO APL1875 G1-RELATED ZINC FINGER PROTEIN (MUS MUSCULUS),
 full insert sequence.
 ACCESSION
 AK008312 GI:12842420
 VERSION
 AK008312.1 HT:CAP trapper.
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 Mus musculus (strain:G57BL/6J) adult male small intestine cDNA to
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 SOURCE
 Mus musculus
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1
 Carninci,P. and Hayashizaki,Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 99279253
 PUBMED
 10349636
 2
 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
 Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 20499374
 PUBMED
 11042159
 3
 Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
 Konno,H., Akiyama,J., Nishi,K., Katsunai,T., Tashiro,H., Itoh,M.,
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 RIKEN integrated sequence analysis (RISA) system--384-format
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 Genome Res. 10 (11), 1757-1771 (2000)
 20530913
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 4
 Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
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DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
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 Site: 2. NotI, Cloned unidirectionally. Primer: Oligo dT.
 Library constructed by Life Technologies. Investigator
 providing samples: Gilbert Smith, NIH"

FEATURES

source

BASE COUNT 294 a 214 c 243 g 244 t 1 others
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 Matches 717; Conservative 0; Mismatches 97; Indels 4; Gaps 4;
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 QY 1253 GTTGAAGATGGATCAGTGTCTTTTACAAGTCCCTGTATCCATGAATATCTAATAGTGC 1312
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 KEYWORDS
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 ORGANISM

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 BI220592
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 Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: c9apbs@mail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM11238 row: n column: 19
 High quality sequence stop: 681.

FEATURES

source

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 Matches 630; Conservative 0; Mismatches 50; Indels 3; Gaps 2;
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 QY 561 CGAATTTACGGTGGCCAGGTTTGGGGAAGCAGCAGTGTCTCTGTTGGCCCTCA 620
 Db 121 CGAATTTACGGTGGCCAGGTTTGGGGAAGCAGCAGTGTCTCTGTTGGCCCTCA 180
 QY 621 TCACAGCGCGCGGGGCTGCACCTTCGCGAGACAGATCCATCTCGCTTATGAGAGATGGG 680
 Db 181 TCACAGCGCGTGGAGGCTGCACCTTCGCGAGACAGATCCATCTCGCTTATGAGAGATGGG 240

GenCore version 5.1.3

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OM nucleic - nucleic search, using sw model

Run on: October 31, 2002, 01:30:37 : Search time 360 Seconds

(without alignments)
11097.347 Million cell updates/sec

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us-09-854-300-7

Perfect score: 1774

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Scoring table:

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Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 20000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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22:	/SID52/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23:	/SID52/gcgdata/geneseq/geneseq-emb1/NA2001R.DAT.*
24:	/SID52/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1773	99.9	1774	AA172095	Human GRAIL cDNA.
2	1662.8	93.7	2773	AAAL5995	Human protein c10n
3	1662.8	93.7	2796	AA172321	ISIGP-4 cDNA. Hom.
4	1431.4	80.7	2876	AA542511	Human cDNA encoding
5	1278.2	72.1	1284	AAAL5985	Human protein c10n
6	1178.8	66.4	2306	AA525884	Human cDNA encoding
7	1167.2	65.8	1249	ABL90796	Human polynucleoti
8	1166	65.7	2145	AA172094	Mouse GRAIL cDNA.
9	1157.5	65.3	1250	AA526340	Human cDNA encoding

10	1106.8	62.4	1287	24	ABK12983	Mouse goliath cDNA
11	1052.4	59.3	1287	24	ABK12992	Synthetic goliath
12	1042.8	58.8	1287	24	ABK12990	Synthetic goliath
13	1042.8	58.8	1287	24	ABK12991	Synthetic goliath
14	1019.4	57.5	1135	22	AA159292	Human polynucleoti
15	999.6	56.3	1287	24	ABK12989	Synthetic goliath
16	977.2	55.1	1287	24	ABK12987	Synthetic goliath
17	972.4	54.8	1287	24	ABK12988	Synthetic goliath
18	655.2	36.9	737	22	AA161078	Human polynucleoti
19	497.2	28.0	502	24	ABN19991	Human ORFX polynuc
20	392.2	22.1	404	22	AAF66696	Novel human polynu
21	372.6	21.0	646	24	ABL38236	Human colon tumour
22	310	17.5	435	24	ABK45625	cDNA encoding colo
23	254.8	14.4	1355	21	AAAB7765	Human secreted pro
24	254.8	14.4	1355	22	AAAF64049	cDNA encoding huma
25	243.8	13.7	918	23	AA570124	DNA encoding novel
26	210.2	11.8	2826	24	ABL90797	Human polynucleoti
27	209	11.8	1200	22	AAF94484	Human hydrophobic
28	209	11.8	1527	22	AAF94494	Human full-length
29	209	11.8	2005	22	AAK94499	Human secreted pro
30	209	11.8	2063	19	AAV43601	Human full-length
31	209	11.8	2452	22	AAK94373	Human secreted pro
32	194.8	11.0	1869	22	ABA09101	Human secreted pro
33	194.8	11.0	1869	22	AAK51507	Human polynucleoti
34	194.8	11.0	1869	22	AAK52491	Human polynucleoti
35	191.8	10.8	1708	23	AA576863	DNA encoding novel
36	180.8	10.2	3615	24	ABK36205	cDNA sequence #596
37	178.8	10.1	631	21	AACT76002	Human ORFX ORF1557
38	149.2	8.4	1322	19	AAV43616	Human secreted pro
39	148.8	8.4	1260	24	ABK12986	Mouse g1 cDNA sequ
40	147.6	8.3	1253	19	AAV40387	Human zinc binding
41	147.6	8.3	1257	22	AAF94418	Human hydrophobic
42	147.6	8.3	1433	22	AAF94428	Human hydrophobic
43	147.6	8.3	1489	24	ABL55072	Human cDNA sequenc
44	147.6	8.3	1515	24	ABL90798	Human polynucleoti
45	147.6	8.3	1546	24	ABL55094	Human cDNA sequenc

ALIGNMENTS

RESULT 1
AA172095
IC AA172095 standard, cDNA; 1774 BP.
XX
AC AA172095;
XX
CT CT-MAP-2002 (first entry)
XX
DE Human GRAIL cDNA.
XX
KW Marine, human, GRAIL, anergy, alteration; tyrosine phosphorylation;
KW antigenic stimulation; interleukin-2; gene therapy; polymorphism, IL-2;
KW anti-immune disease; tumour cell, cancer, transplant rejection, ss.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
CDS 263..1547
FT /*tag= a
FT /product= "GRAIL"
XX
PN WO200185943-A1.
XX
FD 15-NOV-2001.
XX
FF 11-MAY-2001, 2001WO-US15385.
XX
FF 11-MAY-2000, 2000US-203513P.
XX
PA (STED) UNIV LELAND STANFORD JUNIOR.
XX
FI Ford GS, Bloom D, Fatlman CG;

Db 1441 TGAAGCAAAATCTGTGGAGTGATGTTATTCTCTCATGTGNGACACCCACCTTTGAGA 1500
 QY 1501 AGACGAAACTCTTAATCAAGAGACTGCTGTTCGAGAAATTAATCTTAAATCTGTGTAA 1560
 Db 1501 AGACGAAACTCTTAATCAAGAGACTGCTGTTCGAGAAATTAATCTTAAATCTGTGTAA 1560
 QY 1561 ATAGAAAACCTTGAACCATTTAGTAATAACAGAACTGCCAATCAGGGCTAGTTCTATTAA 1620
 Db 1561 ATAGAAAACCTTGAACCATTTAGTAATAACAGAACTGCCAATCAGGGCTAGTTCTATTAA 1620
 QY 1621 TAATTTGATTAATTTAATAAATAAGAGTGAATCTAGTAAAGTCTCAGATGACTAATAT 1680
 Db 1621 TAATTTGATTAATTTAATAAATAAGAGTGAATCTAGTAAAGTCTCAGATGACTAATAT 1680
 QY 1681 ATGCTATAGTTAAATGCTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1740
 Db 1681 ATGCTATAGTTAAATGCTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1740
 QY 1741 TTATAATATTTTTCATAGGCAAGTTTCTCTCAG 1774
 Db 1741 TTATAATATTTTTCATAGGCAAGTTTCTCTCAG 1774

RESULT 2
 ID AAA15995
 XX AAA15995 standard; cDNA: 2773 BP.
 AC AAA15995;
 XX
 DT 12-JUN-2000 (first entry)
 XX
 DE Human protein clone HPI0574 full length coding sequence.
 KW Human protein; hydrophobic domain; nutritional source; haematopoiesis;
 KW cytokine production; cell proliferation; cell differentiation;
 KW immune deficiency; infectious disease; autoimmune disorder; asthma;
 KW multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis;
 KW allergic reaction; osteoporosis; osteoarthritis; periodontal disease;
 KW nervous system disease; Alzheimer's disease; Parkinson's disease;
 KW Huntington's disease; liver fibrosis; lung fibrosis; reperfusion injury;
 KW systemic cytokine damage; tissue differentiation; contraceptive; stroke;
 KW coagulation disorder; myocardial infarction; inflammatory condition;
 KW septic shock; sepsis; ischaemia; reperfusion injury; arthritis; tumour;
 KW nephritis; therapy: ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200005367-A2.
 XX
 PD 03-FEB-2000.
 XX
 PF 22-JUL-1999; 99WO-3F03929.
 XX
 PP 24-JUL-1998; 98JP-0208920.
 PR 07-AUG-1998; 98JP-0224105.
 PR 25-AUG-1998; 98JP-0238116.
 PR 09-SEP-1998; 98JP-0254736.
 PR 29-SEP-1998; 98JP-0275505.
 XX
 PA (SAGA) SAGAMI CHEM RES CENT.
 PA (PROT-) PROTEGENE INC.
 XX
 PI Kato S., Kimura T;
 XX
 DR WPI: 2000-182694/16.
 DR P-PSDB: AAY94897.
 XX
 PT Novel human proteins having hydrophobic domains useful for treating
 PT osteoporosis, Alzheimer's disease, Parkinson's disease, asthma,
 PT multiple sclerosis, rheumatoid arthritis, cancer, anaemia, and stroke -
 XX
 PS Claim 4: Page 348-351; 351pp; English.
 XX

CC This sequence encodes a human protein of the invention, which has
 CC hydrophobic domains. The DNA sequences can be used as a probe or as a
 CC genetic marker. The protein can also be used as a marker, and to identify
 CC potential genetic disorders. The DNA and protein can also be used as
 CC nutritional sources or supplements. The protein exhibits cytokine, cell
 CC proliferation, cell differentiation activities and induces production of
 CC other cytokines in certain cell populations. The protein also exhibits
 CC immune stimulating or immune suppressing activity. It can be used in the
 CC treatment of various immune deficiencies and disorders, and to treat
 CC infectious diseases caused by viral, bacterial, fungal or other
 CC infections. The protein is also used for treating autoimmune disorders
 CC such as multiple sclerosis, systemic lupus erythematosus, and rheumatoid
 CC arthritis. It is also useful in the treatment of allergic reactions and
 CC conditions such as asthma, and in immune suppression after organ
 CC transplantation. The protein is useful in regulation of haematopoiesis
 CC and consequently in the treatment of myeloid or lymphoid cell
 CC deficiencies. It is also used in compositions for tissue growth or
 CC regeneration. The protein is also used in the treatment of osteoporosis
 CC or osteoarthritis and in the treatment of periodontal disease and other
 CC tooth repair processes. The protein is used in the treatment of nervous
 CC system disorders such as Alzheimer's disease, Parkinson's disease, and
 CC Huntington's disease. They are useful for protection or regeneration and
 CC treatment of lung or liver fibrosis, reperfusion injury in various
 CC tissues, and conditions resulting from systemic cytokine damage. They are
 CC also used for promoting or inhibiting tissue differentiation. They are
 CC also used as contraceptives since they exhibit activin or inhibin related
 CC activities and as a fertility inducing therapeutic. They are used for
 CC treating various coagulation disorders and in treatment and prevention of
 CC conditions resulting from coagulation activities e.g. myocardial
 CC infarction or stroke. They also acts as receptors, receptor ligands or
 CC inhibitors or agonists of receptor/ligand interactions. They are used to
 CC treat inflammatory conditions such as septic shock, sepsis, ischaemia
 CC reperfusion injury, arthritis, and nephritis. They can be used to
 CC prevent tumours.
 XX

SQ Sequence 2773 BP: 803 A: 545 C: 617 G: 808 T: 0 other:

Query Match: 93.7%; Score 1662.8; DB 31; Length 2773;
 Best Local Similarity 99.4%; Pred. No. 0;
 Matches 1690; Conservative 0; Mismatches 8; Indels 3; Gaps 2;

QY 74 CCGAGGAGCTGCATCTCGGGCAACCTGTGTGTGAGCGCTACGTGCTCTCGCTCGGACG 133
 Db 22 CCGAGGAGCTGCATCTCGGGCAACCTGTGTGTGAGCGCTACGTGCTCTCGCTCGGACG 81

QY 134 TAGCTCGAGCTCCCGAGCTCCTCACTCCATCTCCCGACCTCGGCGGACCTGCTCAAG 193
 Db 82 TAGCTCGAGCTCCCGAGCTCCTCACTCCATCTCCCGACCTCGGCGGACCTGCTCAAG 141

QY 194 ACTAGGGCTCTCTGCTCAAGCTAGGAGGGGGCTGCGAGGGGGCTAGGGAAGCTGGGAGC 253
 Db 142 ACTAGGGCTCTCTGCTCAAGCTAGGAGGGGGCTGCGAGGGGGCTAGGGAAGCTGGGAGC 201

QY 254 GCGGGGGGGCTATGCGGG 313
 Db 262 GCGGGGGGGCTATGCGGG 261

QY 314 TCCAGATTCCTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 373
 Db 262 TCCAGATTCCTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 321

QY 374 GGGGCTGAAGCTAGTGTGGAGCGGCTACCTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCT 433
 Db 322 GGGGCTGAAGCTAGTGTGGAGCGGCTACCTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCT 381

QY 434 GTGAACCGTACGTGTGGGAGCTGAGCGAGGAGGGGGCTGTACGCCAGAGCTCGCGGCTG 493
 Db 382 GTGAACCGTACGTGTGGGAGCTGAGCGAGGAGGGGGCTGTACGCCAGAGCTCGCGGCTG 441

QY 494 GAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 553
 Db 442 GAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 501

QY	134	TAGCTCGACGCTCCCGAGTCTCAGTCTCCATTCCTCCACGCTGGCGGCACCTGCTCAAG	193
Db	88	TAGCTCGACGCTCCCGAGTCTCAGTCTCCATTCCTCCACGCTGGCGGCACCTGCTCAAG	147
QY	194	ACCAGGGTCTGCCAAGCCTAGGAGGCGCTGCCAGGGCGCTAGGGAACCTGCGGAGC	253
Db	148	ACCAGGGTCTGCCAAGCCTAGGAGGCGCTGCCAGGGCGCTAGGGAACCTGCGGAGC	207
QY	254	GGCGGGCCATGGGCGCGCGCTGGGCGCGGGGTCTCTGCGCGGGTGGCTGGGCTTT	313
Db	208	GGCGGGCCATGGGCGCGCGCTGGGCGCGGGGTCTCTGCGCGGGTGGCTGGGCTTT	267
QY	314	TCCAGATTGCTGCGATGCTGCTCTGCTGCGGCTGAGTCCGCGAGCACCGGCTTCCGG	373
Db	268	TCCAGATTGCTGCGATGCTGCTCTGCTGCGGCTGAGTCCGCGAGCACCGGCTTCCGG	327
QY	374	GGGGCTGAGAGCTGTGGACCGCGTACGCTCAACGTGTCCTGCGGGTTCGCCACCGGA	433
Db	328	GGGGCTGAGAGCTGTGGACCGCGTACGCTCAACGTGTCCTGCGGGTTCGCCACCGGA	387
QY	434	GTCAAGCTGACGCTGGGAGCTGAGCGAGGAGGCGGTGTACGGCCAGGACTCCGCGCTG	493
Db	388	GTCAAGCTGACGCTGGGAGCTGAGCGAGGAGGCGGTGTACGGCCAGGACTCCGCGCTG	447
QY	494	GAGCCTGTGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	553
Db	448	GAGCCTGTGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	507
QY	554	CCGCACAGAAATTCACGCTGCCACGGTTTGGGGAAGCACCGTGCACAGTCTCTTGCTG	613
Db	508	CCGCACAGAAATTCACGCTGCCACGGTTTGGGGAAGCACCGTGCACAGTCTCTTGCTG	567
QY	614	GCCTCATCCACGGCGGGGCTGCACCTTCGCGAGACAGATCCATCTCGCTTATGAG	673
Db	568	GCCTCATCCACGGCGGGGCTGCACCTTCGCGAGACAGATCCATCTCGCTTATGAG	627
QY	674	AGATGGCGCTGTGAGCGCTCATCTTTAACTTCCCGCGGACCGCGCAATGAGTCAATCCC	733
Db	628	AGATGGCGCTGTGAGCGCTCATCTTTAACTTCCCGCGGACCGCGCAATGAGTCAATCCC	687
QY	734	ATGCTCTCACCGGGTGCAGTACATCTGTTGCAATCATGATCGCGCAATCTGAAAGGACA	793
Db	688	ATGCTCTCACCGGGTGCAGTACATCTGTTGCAATCATGATCGCGCAATCTGAAAGGACA	747
QY	794	AAATCTCTCAATCTATTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	853
Db	748	AAATCTCTCAATCTATTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	807
QY	854	AAACATGGCCCTTGGGTGAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT	913
Db	808	AAACATGGCCCTTGGGTGAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT	867
QY	914	ATTACGGCGGCACTGTGGCTATTTATCTTTTATCTCTCCAGCGCTACGCAATGCA	973
Db	868	ATTACGGCGGCACTGTGGCTATTTATCTTTTATCTCTCCAGCGCTACGCAATGCA	927
QY	974	AGAGCTCAAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1033
Db	928	AGAGCTCAAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	987
QY	1034	CTTCACTACGCTACAGTGAACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1093
Db	988	CTTCACTACGCTACAGTGAACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1047
QY	1094	GCTGTGCTGATTTGATTAACCAATGATTTGGTACGCTCTTAACGCTGCAACCAT	1153
Db	1048	GCTGTGCTGATTTGATTAACCAATGATTTGGTACGCTCTTAACGCTGCAACCAT	1107
QY	1154	ATTTCCATTAAGACATGTGTTGACGCTATGCTGTGTTTAAACCAATTAAGACATGCT	1213
Db	1108	ATTTCCATTAAGACATGTGTTGACGCTATGCTGTGTTTAAACCAATTAAGACATGCT	1167

QY	1214	AAATGTGACATCTCAAGAGCTTTGGGAATTTGAGGTGGATGTTGAGATGGATGATGCT	1273
Db	1168	AAATGTGACATCTCAAGAGCTTTGGGAATTTGAGGTGGATGTTGAGATGGATGATGCT	1227
QY	1274	TTACAAGTCCCTGTATCCCAATGAAATATCTAATAGTCCCTCTCCCATGAAGAGATAA	1333
Db	1228	TTACAAGTCCCTGTATCCCAATGAAATATCTAATAGTCCCTCTCCCATGAAGAGATAA	1287
QY	1334	CGCAGGAGACGCTGATCATCTGATATGCTTCAGTACAGGGAACAGATGACCCGCTCTG	1393
Db	1288	CGCAGGAGACGCTGATCATCTGATATGCTTCAGTACAGGGAACAGATGACCCGCTCTG	1347
QY	1394	GAGGAACAGCTGCACTCAACAAATGAAAGTCTACAGCTGGTAAACCATGAAGCAAAATCT	1453
Db	1348	GAGGAACAGCTGCACTCAACAAATGAAAGTCTACAGCTGGTAAACCATGAAGCAAAATCT	1407
QY	1454	GTGGCAGTGGATGTTTATTCCTCATGTNGACACCAACCTTTTGAAGAGAGCAAACTCT	1513
Db	1408	GTGGCAGTGGATGTTTATTCCTCATGTNGACACCAACCTTTTGAAGAGAGCAAACTCT	1467
QY	1514	AATCAAGAGACTGCTGTTTCGAGAAATTAATCTTAAATCTGTGTAAATAGAAACTTGA	1573
Db	1468	AATCAAGAGACTGCTGTTTCGAGAAATTAATCTTAAATCTGTGTAAATAGAAACTTGA	1527
QY	1574	ACCATAGTAAATAACAGAACTGCCAATCAGGCGCTAGTTTCTTAAATAATGGATAAA	1633
Db	1528	ACCATAGTAAATAACAGAACTGCCAATCAGGCGCTAGTTTCTTAAATAATGGATAAA	1587
QY	1634	TTTAATAAATAAGAGTGTATCTGAAAGTGTCTAGATGACTAATATATGCTATAGTAA	1693
Db	1588	TTTAATAAATAAGAGTGTATCTGAAAGTGTCTAGATGACTAATATATGCTATAGTAA	1647
QY	1694	AATGGCTTAAATAATTTAACTGTAACTTTTCCACCAACTCATTATATATTTT	1753
Db	1648	A--TGCTTAAATAATTTAACTGTAACTTTTCCCA--CAACTCATTATATATTTT	1704
QY	1754	CATAGCAAGTTTCTCTCAG	1774
Db	1705	CATAGCAAGTTTCTCTCAG	1725

RESULT 4

AAS42511

ID AAS425.1 standard: cDNA: 2876 BP.

XX

AC AAS42511;

XX

DT 18-DEC-2001 (first entry)

XX

Human cDNA encoding an mddt protein, clone LI:757439.1:2000MAY01.

Human: molecules for disease detection and treatment; mddt; ss;
 Antiarteriosclerotic; hepatotropic; antipsoriatic; cytostatic;
 immunosuppressive; antidiabetic; antiasthmatic; neuroprotective;
 osteopathic; antirheumatic; cell proliferative disorder;
 arteriosclerosis; cirrhosis; psoriasis; cancer; adenocarcinoma;
 leukaemia; breast cancer; autoimmune disorder; AIDS;
 acquired immunodeficiency syndrome; Addison's disease;
 diabetes mellitus; asthma; multiple sclerosis; osteoarthritis.

XX Homo sapiens.

OS

XX

XX WO200162922-A2.

PN

XX

PD 30-AUG-2001.

XX

XX 21-FEB-2001; 2001WO-US05896.

XX

XX 24-FEB-2000; 2000US-0185213.

PR

PR 16-MAY-2000; 2000US-0205232.

PR

PR 17-MAY-2000; 2000US-0205285.

PR

PR 17-MAY-2000; 2000US-0205286.

PR

PR 17-MAY-2000; 2000US-0205287.


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Db 661 GCAACTGCGGTATTTATCTTTATCTGTTGTAAGATGCAAGAGCTGAA 720
QY 983 AGCAGGAAGCAGAGCGCAATTAAGGCAGATGCTAAAAAGAGTATTGGAGGCTTCAACTA 1042
Db 721 AGCAGGAAGCAGAGCGCAATTAAGGCAGATGCTAAAAAGAGTATTGGAGGCTTCAACTA 780
QY 1043 CGCACACTGAACCAAGGACAGCAAGAAATTGGCCCTGATGAGATAGTTGCTGTGTGGC 1102
Db 781 CGTAAATTAAGCAAGGACAGCAAGAAATTGGCCCTGATGAGATAGTTGCTGTGTGGC 840
QY 1103 ATTAAATTTATAAATTAATGATTTGATGATGATTTTAAAGTGTAAACATATTTTCAAT 1162
Db 841 ATTAAATTTATAAATTAATGATTTGATGATGATTTTAAAGTGTAAACATATTTTCAAT 900
QY 1163 AAACATGTTTGAAGGATGATGATTTTAAACACAGCAATTTGCTGATGATGATGATGAT 1222
Db 901 AAGACATGTTTGAAGGATGATGATTTTAAACACAGCAATTTGCTGATGATGATGATGAT 960
QY 1223 ATACTCAAAAGCTTTGCAAGTTCAGCTGATGATGATGATGATGATGATGATGATGATGAT 1282
Db 961 ATACTCAAAAGCTTTGCAAGTTCAGCTGATGATGATGATGATGATGATGATGATGATGAT 1020
QY 1283 GCTTATATTAATTAATATTAATATTAATATTAATATTAATATTAATATTAATATTAAT 1342
Db 1021 GCTTATATTAATTAATATTAATATTAATATTAATATTAATATTAATATTAATATTAAT 1080
QY 1343 ACCGATCATGTCGATATGTCATGATGATGATGATGATGATGATGATGATGATGATGAT 1402
Db 1081 AATGATCATGTCGATATGTCATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
QY 1403 GTGATGATCAAAATCAAAAGTTCAGCTGATGATGATGATGATGATGATGATGATGATGAT 1462
Db 1141 GTGATGATCAAAATCAAAAGTTCAGCTGATGATGATGATGATGATGATGATGATGATGAT 1200
QY 1463 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1522
Db 1201 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
QY 1523 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1582
Db 1261 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320

RESULT 6
AAS25884
ID AAS25884 standard, cDNA, 2306 BP.
XX AAS25884.
XX
XX 07-NOV-2001 (first entry)
XX
XX Human cDNA encoding a novel secreted protein. Seq ID #1
XX
XX Human, immunosuppressive, antirheumatic, ss, antirheumatic,
XX cytostatic, cardiant, vasotropic, cerebroprotective, neurotropic,
XX neuroprotective, antibacterial, virucidal, fungicidal, ophthalmological,
XX vulnary; secreted protein; rheumatoid arthritis;
XX hyperproliferative disorder; cardiovascular disorder; cardiac arrest;
XX cerebrovascular disorder; cerebral ischaemia; angiogenesis;
XX nervous system disorder; Alzheimer's disease; infection; ocular disorder;
XX corneal infection; wound healing; epithelial cell proliferation;
XX skin ageing; food additive, preservative, antiproliferative.
XX
XX Homo sapiens.
XX
XX WC2001F122-A2
XX
XX 02-AUG-2001
XX
XX 17-JAN-2001, 2001W05U141.
XX
XX 31-JAN-2000, 2000US-017905.
XX

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PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215115.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 14-AUG-2000; 2000US-0225779.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226688.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 09-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234497.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.

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PR 02-OCT-2000: 2000US-0237038.
 PR 02-OCT-2000: 2000US-0237039.
 PR 02-OCT-2000: 2000US-0237040.
 PR 13-OCT-2000: 2000US-0239935.
 PR 13-OCT-2000: 2000US-0239937.
 PR 20-OCT-2000: 2000US-0240960.
 PR 20-OCT-2000: 2000US-0241221.
 PR 20-OCT-2000: 2000US-0241785.
 PR 20-OCT-2000: 2000US-0241786.
 PR 20-OCT-2000: 2000US-0241787.
 PR 20-OCT-2000: 2000US-0241808.
 PR 20-OCT-2000: 2000US-0241809.
 PR 20-OCT-2000: 2000US-0241826.
 PR 01-NOV-2000: 2000US-0244617.
 PR 08-NOV-2000: 2000US-0246474.
 PR 08-NOV-2000: 2000US-0246475.
 PR 08-NOV-2000: 2000US-0246476.
 PR 08-NOV-2000: 2000US-0246477.
 PR 08-NOV-2000: 2000US-0246478.
 PR 08-NOV-2000: 2000US-0246523.
 PR 08-NOV-2000: 2000US-0246524.
 PR 08-NOV-2000: 2000US-0246525.
 PR 08-NOV-2000: 2000US-0246526.
 PR 08-NOV-2000: 2000US-0246527.
 PR 08-NOV-2000: 2000US-0246528.
 PR 08-NOV-2000: 2000US-0246532.
 PR 08-NOV-2000: 2000US-0246609.
 PR 08-NOV-2000: 2000US-0246610.
 PR 08-NOV-2000: 2000US-0246611.
 PR 08-NOV-2000: 2000US-0246613.
 PR 17-NOV-2000: 2000US-0249207.
 PR 17-NOV-2000: 2000US-0249208.
 PR 17-NOV-2000: 2000US-0249209.
 PR 17-NOV-2000: 2000US-0249210.
 PR 17-NOV-2000: 2000US-0249211.
 PR 17-NOV-2000: 2000US-0249212.
 PR 17-NOV-2000: 2000US-0249213.
 PR 17-NOV-2000: 2000US-0249214.
 PR 17-NOV-2000: 2000US-0249215.
 PR 17-NOV-2000: 2000US-0249216.
 PR 17-NOV-2000: 2000US-0249217.
 PR 17-NOV-2000: 2000US-0249218.
 PR 17-NOV-2000: 2000US-0249244.
 PR 17-NOV-2000: 2000US-0249245.
 PR 17-NOV-2000: 2000US-0249264.
 PR 17-NOV-2000: 2000US-0249265.
 PR 17-NOV-2000: 2000US-0249297.
 PR 17-NOV-2000: 2000US-0249299.
 PR 17-NOV-2000: 2000US-0249300.
 PR 01-DEC-2000: 2000US-0250160.
 PR 01-DEC-2000: 2000US-0250191.
 PR 05-DEC-2000: 2000US-0251030.
 PR 05-DEC-2000: 2000US-0251988.
 PR 05-DEC-2000: 2000US-0251989.
 PR 06-DEC-2000: 2000US-0251479.
 PR 08-DEC-2000: 2000US-0251856.
 PR 08-DEC-2000: 2000US-0251868.
 PR 08-DEC-2000: 2000US-0251869.
 PR 08-DEC-2000: 2000US-0251989.
 PR 11-DEC-2000: 2000US-0251990.
 PR 11-DEC-2000: 2000US-0254097.
 PR 05-JAN-2001: 2001US-0259678.
 (HUMA-) HUMAN GENOME SCI INC.

PA Rosen CA, Barash SC, Ruben SM;
 PI
 XX
 DR WPI: 2001-488783/53.
 DR P-PSDB; AAU15897.

XX New nucleic acid molecules encoding 461 human secreted proteins for
 PT diagnosing, preventing, treating or ameliorating medical conditions and
 PT used as food additives or preservatives -

XX

Claim 1: SEQ ID NO 63: 980pp: English.

PS

XX

The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acid and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunoassays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection, and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence encodes a novel secreted protein of the invention.

Query Match 66.4%; Score 1178.8; DB 22; Length 2306;
 Best Local Similarity 99.0%; Pred. No. 0;
 Matches 1217; Conservative 0; Mismatches 8; Indels 4; Gaps 3;

OY

547 CTGTAACCCGCGACAGCAATTTTCACGGTGCCTCCACGGTTTGGGGAAGCACCCTGCAAGTCTC 606
 12 CTGTAACCCGCGACAGCAATTTTCACGGTGCCTCCACGGTTTGGGGAAGCACCCTGCAAGTCTC 71
 607 TTGTTGGTGGTCTCATCCACGCGGGGGGCTGCACCTTCGCACAGCAAGATCCATCTGGC 666
 72 TTGTTGGTGGTCTCATCCACGCGGGGGGCTGCACCTTCGCACAGCAAGATCCATCTGGC 131
 667 TTATGAGAGATGCGCGTCTGAGCGGTCTATTTAACTTTCCTGGGAGCTGGCAATGAGGT 726
 132 TTATGAGAGAGCGGGGTCTGAGTGTCTATTTAACTTTCCTGGGAGCTGGCAATGAGGT 191
 727 CATCCCATGCTCATCCCGGGTGCAGTAGACATTTGTCACATCATGTCGCAATCTGAA 786
 192 CATCCCATGCTCATCCCGGGTGCAGTAGACATTTGTCACATCATGTCGCAATCTGAA 251
 787 AGGCACAAAATTTCTGCAATCTATTCAAAGAGGCATACAGTGCATGATGATGATGATGAT 846
 252 AGGCACAAAATTTCTGCAATCTATTCAAAGAGGCATACAGTGCATGATGATGATGATGAT 311
 847 AGGGAAGAAACATGCGCTTGGTGAATCAGTATTCATGCTGCTGCTGCTGCTGCTGCTGCT 905
 312 AGGGAAGAAACATGCGCTTGGTGAATCAGTATTCATGCTGCTGCTGCTGCTGCTGCTGCT 371
 906 TTTTATTATTACGGCGCACTGTGGGTATTTTATCTTTTATCTGCTGCTGCTGCTGCTGCTGCT 965
 372 TTTTATTATTACGGCGCACTGTGGGTATTTTATCTTTTATCTGCTGCTGCTGCTGCTGCTGCT 431
 965 GGAATGCAAGAGCTCAAG 1025
 432 GGAATGCAAGAGCTCAAG 491
 1026 TTGGAGAGCTTCACTAGCAGCAGTGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1085
 492 TTGGAGAGCTTCACTAGCAGCAGTGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 551
 1086 ATAGTTGTGCTGTGTGCTATGAATTTGATAACCAAAATGATTTGGTACGATCTTAACGT 1145
 552 ATAGTTGTGCTGTGTGCTATGAATTTGATAACCAAAATGATTTGGTACGATCTTAACGT 611
 1146 GCAACCATATTTTCCATAGACATGTGTTGACCATGCTGTTAAAAACACAAGACTTGCC 1205

1b 612 GACACATATATTTCCATAAAGACATGTTGTAACCATGCTGTTAGAACACAGACCTGCG 671
 Qy 1206 CCATGTCGAATGTGACATACCTCAAGCTTTGGGAATTAAGTGGATGAT 1265
 Db 672 CCAATGTCGAATGTGACATACCTCAAGCTTTGGGAATTAAGTGGATGAT 731
 Qy 1266 CAGTGTCTTTACAGTCCCTGTATCCAAATGAATATCTAATAGTGCCTCCCTCCCATGAAG 1325
 Db 732 CAGTGTCTTTACAGTCCCTGTATCCAAATGAATATCTAATAGTGCCTCCCTCCCATGAAG 791
 Qy 1326 AGSATAATGAGCGAGACGATCATCTGGATATCTTACATACAGGGAACAGATGAAC 1385
 Db 792 AGGATAATGAGCGAGACGATCATCTGGATATCTTACATACAGGGAACAGATGAAC 851
 Qy 1386 CGCTCTGGAGACACAGTGCATCAACAAATGAAGTGTACAGCTGTAAACCATGAAG 1445
 Db 852 CGCTCTGGAGACACAGTGCATCAACAAATGAAGTGTACAGCTGTAAACCATGAAG 911
 Qy 1446 CAATTTCTGGAGTGGATGATTTCTTCATCTGACAGCAACCAACCTTTGAAGAGAG 1505
 Db 912 CAATTTCTGGAGTGGATGATTTCTTCATCTGACAGCAACCAACCTTTGAAGAGAG 971
 Qy 1506 AAATCTCTATCAAGACAGCTGCTGTCGAGAAATTAATCTTAAATCTGTCTAATAGA 1565
 Db 972 AAATCTCTATCAAGACAGCTGCTGTCGAGAAATTAATCTTAAATCTGTCTAATAGA 1031
 Qy 1566 AAATCTCTATCAAGACAGCTGCTGTCGAGAAATTAATCTTAAATCTGTCTAATAGA 1625
 Db 1032 AAATCTCTATCAAGACAGCTGCTGTCGAGAAATTAATCTTAAATCTGTCTAATAGA 1091
 Qy 1626 TGGATAATTTAATAAATGAAGTGTATCTGACAGTGTGACATTAATATGCT 1685
 Db 1092 TGGATAATTTAATAAATGAAGTGTATCTGACAGTGTGACATTAATATGCT 1151
 Qy 1686 ATAGTTAAATGGCTTAAATATTTAACTGTGTTAACTTTTCCACCAACATCATATA 1745
 Db 1152 ATAGTTAAATGGCTTAAATATTTAACTGTGTTAACTTTTCCACCAACATCATATA 1208
 Qy 1746 ATATTTTCTAGGCAAGTTTCTCTCTCAG 1774
 Db 1209 ATATTTTCTAGGCAAGTTTCTCTCTCAG 1237

RESULT 7
 ABL90796
 ID ABL90796 standard; cDNA; 1249 BP.
 XX AC ABL90796;
 XX ET 24-MAY-2002 (first entry)
 XX DE Human polynucleotide SEQ ID NO 1358.
 XX KW Cytostatic, immunosuppressive, neurotropic, neuro-protective, antiviral,
 KW antiallergic, hepatotropic, antidiabetic, antiinflammatory, antiulcer,
 KW vulnerary, anticonvulsant, antibacterial, antifungal, antiparasitic,
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein; gene; ss
 XX OS Homo sapiens.
 XX PN WO2000190304-A2.
 XX PD 29-NOV-2001.
 XX PF 18-MAY-2001; 2001WO-US16450.
 XX PR 19-MAY-2000; 2000US-205515P.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Birse CE, Rosen CA;

XX WFL: 3002-122018/16.
 DR P-PSDB; ABB90387.
 XX Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders -
 XX Claim 4: SEQ ID NO 1358; 2081pp + Sequence Listing; English.
 XX The invention relates to novel genes (ABLR9449-ARI90853) and proteins (ABBR9040-ABBR9044) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 1249 BP; 379 A; 258 C; 273 G; 335 T; 4 other:
 Qy Query Match 65.8%; Score 1167.2; DB 24; Length 1249;
 Db Best local similarity 98.7%; Pred. NO. 2.2e-314;
 Qy Matches 1206; Conservative 1; Mismatches 11; Indels 4; Gaps 3;

Qy 547 CTGTACCCGCGACAGCAATTTCCAGTGCCTCCAGGTTTGGGGAACGCGTGCACACTCTC 606
 Db 18 CTGTACCCGCGACAGCAATTTCCAGTGCCTCCAGGTTTGGGGAACGCGTGCACACTCTC 77
 Qy 607 TTGTTGGGCTCATCAAGCGGCGGCGGCTGCACTTTGCTAGATGATCATCTGAC 666
 Db 78 TTGTTGGGCTCATCAAGCGGCGGCGGCTGCACTTTGCGAGACAGATCATCTGCG 137
 Qy 667 TTATGAGAGATGGCGCTCTGGAGCGCTCATCTTTAACTTCCCGGAGCCCGCAATGAGT 726
 Db 138 TTATGAGAGATGGCGCTCTGGAGCGCTCATCTTTAACTTCCCGGAGCCCGCAATGAGT 197
 Qy 727 CATCCCGATGCTCACCGCGGCTGCACTGACATCTGTCATCATGATGATGATGATGAT 786
 Db 194 CATCCCGATGCTCACCGCGGCTGCACTGACATCTGTCATCATGATGATGATGATGAT 257
 Qy 787 AGGCACAAAAATTTCTGCAATCTATTCAAGAGGATACAGTACATGATGATGATGATGAT 846
 Db 258 AGGCACAAAAATTTCTGCAATCTATTCAAGAGGATACAGTACATGATGATGATGATGAT 317
 Qy 847 AGGCAAAAAATGCGCTTGGTGAATCACTATCTCAATTTTTCGTTTCTGCTGCTT 906
 Db 318 AGGCAAAAAATGCGCTTGGTGAATCACTATCTCAATTTTTCGTTTCTGCTGCTT 377
 Qy 907 TTTTATTTATACGCGGCAACTGTGGCTATTTTATCTTTTATCTGCTGCAAGGCTAGG 966
 Db 378 TTTTATTTATACGCGGCAACTGTGGCTATTTTATCTTTTATCTGCTGCAAGGCTAGG 437
 Qy 967 GAATGCAAGAGCTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1026
 Db 438 GAATGCAAGAGCTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 497
 Qy 1027 TGGAGGCTTCAACTACGACACTGAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1085
 Db 498 TGGAGGCTTCAACTACGACACTGAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 557
 Qy 1086 ATAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1145

Matches 1208:		Conservative	0:	Mismatches	10:	Indels	5:	Gaps	4:
QY	547	CTGTAACCCGACACGAATTTACAGCTGCCAGCTTTGGGAAACACCGTCCAGCTC	606						
Db	18	CTGTAACCCGACACGAATTTACAGCTGCCAGCTTTGGGAAACACCGTCCAGCTC	77						
QY	607	TTGGTTGGGCTTCATCAAGCGGCGGCGGCTGCACTTTGGCAGACAAAGATCCATCTGGC	666						
Db	78	TTGGTTGGGCTTCATCAAGCGGCGGCGGCTGCACTTTGGCAGACAAAGATCCATCTGGC	137						
QY	667	TTATGACAGATGGGCTCTGGAGCTGCTCATCTTTAACTTCCCGGAGACCCCAATGAGGT	726						
Db	138	TTATGAGAGAGGGGCTCTGGAGCGCTCATCTTTAACTTCCCGGAGACCCCAATGAGGT	197						
QY	727	CATCCCATCTCTACCCGCGGTGAGTAGACATTTGTCATCATGATGAGTCAATCTGAA	786						
Db	198	CATCCCATCTCTACCCGCGGTGAGTAGACATTTGTCATCATGATGAGTCAATCTGAA	247						
QY	787	AGGCACAAAATTTCTCAATCTATTCCAAAGAGCGCATAGAGTGCATAGAGT	846						
Db	258	AGGCACAAAATTTCTCAATCTATTCCAAAGAGCGCATAGAGTGCATAGAGT	317						
QY	847	AGGAAAAAATCATGGCCCTTGGTGAATCACTATTCAA-TTTTTTCGTTTCTGTGCT	905						
Db	318	AGGAAAAAATCATGGCCCTTGGTGAATCACTATTCAA-TTTTTTCGTTTCTGTGCT	377						
QY	906	TTTTTATTATAGCGGCGCACTGTGGCTATTTTATCTTTATCTGCTCGAAGGCTAC	965						
Db	378	TTTTTATTATAGCGGCGCACTGTGGCTATTTTATCTTTATCTGCTCGAAGGCTAC	437						
QY	966	GGATGCAAGAGCTCAAGACAGGACGAGCGCAATTTAAGCGAGATGCTAAAAAGCTA	1025						
Db	438	GGATGCAAGAGCTCAAGACAGGACGAGCGCAATTTAAGCGAGATGCTAAAAAGCTA	497						
QY	1026	TTGGAAGGCTTCAACTACGCACCTGAAACAGGAGAGCAAG-AAAATTGGCCCTGATGGA	1084						
Db	498	TTGGAAGGCTTCAACTACGCACCTGAAACAGGAGAGCAAG-AAAATTGGCCCTGATGGA	557						
QY	1085	GATAGTTGCTGTGTGCATTTGAATTTGTAATAACCAATGATTTGGTACGCATCTTAACG	1144						
Db	558	GATAGTTGCTGTGTGCATTTGAATTTGTAATAACCAATGATTTGGTACGCATCTTAACG	617						
QY	1145	TGCAACCATATTTTCCATAGACATGCTTGACCGATGCTTAAACACCAACACTTGC	1204						
Db	618	TGCAACCATATTTTCCATAGACATGCTTGACCGATGCTTAAACACCAACACTTGC	677						
QY	1205	CCCATGTGCAAAATGTGACATCTCAAAAGCTTTGGGAATTTGAGTGTGATGTTGAAGATGGA	1264						
Db	678	CCCATGTGCAAAATGTGACATCTCAAAAGCTTTGGGAATTTGAGTGTGATGTTGAAGATGGA	737						
QY	1265	TCAGTGTCTTTACAGTCTCTGTATCCCAATGAATATATCTATAGTGGCTCTCCCATGAA	1324						
Db	738	TCAGTGTCTTTACAGTCTCTGTATCCCAATGAATATATCTATAGTGGCTCTCCCATGAA	797						
QY	1325	GAGGATAATCGGACGAGACCGCATCTGATGATGCTTCAGTACAGGGAAACAGATGAA	1384						
Db	798	GAGGATAATCGGACGAGACCGCATCTGATGATGCTTCAGTACAGGGAAACAGATGAA	857						
QY	1385	CCGCTCTCTGAGAAACATGCAATGCAATGAATGAATGAACTGTACAGCTGGTAAACCATGAA	1444						
Db	858	CCGCTCTCTGAGAAACATGCAATGCAATGAATGAATGAACTGTACAGCTGGTAAACCATGAA	917						
QY	1445	GCAATCTCTGGCAGTGTATTTATCTCATGTNGACACCCCACTTTGAGAGACAC	1504						
Db	918	GCAATCTCTGGCAGTGTATTTATCTCATGTNGACACCCCACTTTGAGAGACAC	977						
QY	1505	GAACTCTCTAATCAAGAGACTGCTGTGAGAAATTTAAATCTTAAATCTGTGTAATAG	1564						
Db	978	GAACTCTCTAATCAAGAGACTGCTGTGAGAAATTTAAATCTTAAATCTGTGTAATAG	1037						
QY	1565	AAAATTGACCATTTAGTAATAACAGAACTGCTAATTAATTAATTAATAA	1624						
Db	1038	AAAATTGACCATTTAGTAATAACAGAACTGCTAATTAATTAATTAATAA	1697						

QY 1625 TTGGATAAATTTAATAAATAAGAGTGTACTAGAAAGTCTCAGATGACTAATATTATGC 1684
 Db 1098 TTGGATAAATTTAATAAATAAGAGTGTACTAGAAAGTCTCAGATGACTAATATTATGC 1157
 QY 1685 TATAGTAAATTTGGCTTTAAATAATTTAACTGTTAACTTTTTTCCACCAAACTCATTAT 1744
 Db 1158 TATAGTAAATTTGGCTTTAAATAATTTAACTGTTAACTTTTTTCCCA-CAAACTCATTAT 1214
 QY 1745 AATATTTTTCATAGGCAAGTTTC 1767
 Db 1215 AATATTTTTCATAGGCAATTTCC 1237

RESULT 10

ABK12983

ID ABK12983 standard, cDNA, 1287 BP.

XX ABK12983;

AC AC

DT 23-APR-2002 (first entry)

XX Mouse goliath cDNA sequence.

DE Mouse goliath cDNA sequence.

XX Mouse goliath protein; antiangiogenic; vasotropic; gene therapy;

KW dosage form; angiogenesis; neurogenesis; tumour; vascularisation;

KW cancer; ischaemia; neuroblastoma; neurodegenerative disease;

KW unrecovered nerve trauma; gene, ss.

XX Mus sp.

OS Mus sp.

XX Key

FH Location/Qualifiers

FT 1..1287

FT CDS

FT /*tag= a

FT /product= "Mouse_goliath_protein"

XX WO2001093681-A1.

PD 13-DEC-2001.

XX 01-JUN-2001; 2001WO-US18000.

XX 02-JUN-2000; 2000US-0586399.

XX (REGC) UNIV CALIFORNIA.

XX Harland R, Baker JC;

XX WPI, 2002-147637/19.

XX P-PSDB; AAU74918.

XX New compositions comprising goliath proteins, useful for modulating

PT angiogenesis or neurogenesis in mammals e.g. for preventing or

PT treating undesirable vascularisation of a tumour, ischaemia or

PT neurodegenerative disease

XX Examples, Page 38, 45pp, English.

XX The present invention relates to a new pharmaceutical composition that

CC comprises a goliath polypeptide in dosage form. The goliath polypeptide

CC has a sequence identity of at least 75% to the protein sequences

CC (AAU74918-AAU74921) fully defined in the specification. The composition

CC is useful for modulating angiogenesis or neurogenesis in mammals,

CC particularly in humans or mice. Specifically, the composition is useful

CC for the prophylactic and/or therapeutic treatment of excess angiogenesis

CC e.g. undesirable vascularisation of a tumour or insufficient angiogenesis

CC e.g. ischaemia, excess neurogenesis e.g. neuroblastoma or insufficient

CC neurogenesis e.g. neurodegenerative disease or unrecovered nerve trauma.

CC The present nucleic acid sequence encodes the mouse goliath protein

CC that was used in the invention for modulating angiogenesis or

CC neurogenesis.

XX Sequence 1287 BP, 308 A, 320 C, 359 G, 300 T, 0 other;

CC ABK12992; used in the invention for modulating angiogenesis or
 CC neurogenesis.

XX Sequence 1287 BP: 312 A, 321 C, 356 G, 298 T; 0 other;

Query Match 58.8%; Score 1042.8; DB 24; length 1287.
 Best Local Similarity 88.1%; Pred No 8 7-280.
 Matches 1134; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

QY 263 ATGGGGCGCGCGCTGGGGCGGGCTTCCTGGCGCGGGTGGCTCGCGCTTTTCAGATG 322
 Db 1 ATGGGGCGCGCGCGGGATAGGGGTCTACTGGCGCGGGTGGCTCGCGGCTTGC 60
 QY 323 CTGGCATGCTGCT 382
 Db 61 CTGGCTGTGTCT 120
 QY 383 CGATGTGGACGGGTACCTCAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 442
 Db 121 GCGGTGTGACCGCGTACCTCAACCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
 QY 443 AGCGCTGGAGCTGAGCGAGCGGGCGGTCTACGGCGAGGCTAGCGCTGGAG 502
 Db 181 ACTGTGGGAGCTGAGCGAGCGGGCGGTCTACGGCGAGGCTAGCGCTGGAG 240
 QY 503 GTGGGGTGTGTGTATCTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGT 562
 Db 241 TCGGGGTCTGTGTTCGGCGCGAGCGGGGTGTGGGGTGTGGGGTGTGGGGT 600
 QY 563 AATTTACGGTCT 622
 Db 301 AATTTACAGTCT 360
 QY 623 CAACGGGGGGGGTGTGACCTCTGACACAGATCTGCTGCTTATGAGAGTGGCG 682
 Db 361 CACGGGGTGGAGCTGACATCTCGGACAGATCTGCTGCTTATGAGAGTGGCG 420
 QY 683 TCTGGAGCGTCT 742
 Db 421 TCTGGAGCGTCT 480
 QY 743 CCGGGTGCAGTACAGATCTGTCATCATGATCGGCAATCTGAAAGGCACAAAATCTG 802
 Db 481 CCGGGTGCAGTACAGATCTGTCATCATGATCTGAAAGGCACAAAATCTG 540
 QY 803 CAATCTATTCAAGAGGATCAAGTACATGCTATAGAGTGGGAAAGAAATCTGC 862
 Db 541 CATCTATTCAAGAGGATCAAGTACATGCTATAGAGTGGGAAAGAAATCTGC 600
 QY 863 CTTGGGTGAATCAATCAATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 922
 Db 601 CTTGGGTGAATCAATCAATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 660
 QY 923 GCACGTGGGTATTATCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 982
 Db 661 GCACGTGGGTATTATCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
 QY 983 AGCAGGAACAGAGTAAATTAAGATAGATTAAGAAATATTTGAAAGTCTTCAACTA 1042
 Db 721 AGCAGGAACAGAGTAAATTAAGATAGATTAAGAAATATTTGAAAGTCTTCAACTS 780
 QY 1043 CGCACATCAACACAGGACACAGAAATATGATGATGATGATGATGATGATGAT 1102
 Db 781 CGCACATCAACACAGGACACAGAAATATGATGATGATGATGATGATGATGAT 840
 QY 1103 ATGGAATGATTAACCAATATTTGATGATGATGATGATGATGATGATGATGAT 1162
 Db 841 ATGGAATGATTAACCAATATTTGATGATGATGATGATGATGATGATGATGAT 900
 QY 1163 AGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1222
 Db 901 AATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960

QY 1223 ATACTCAAGCTTTGGGAATTGAGTGGATGCTTCAAGATGATCAGTGTCTTTACAGTC 1282
 Db 961 ATTCTCAAGCTCTTGGGAATTGAGTGGATGCTTCAAGATGATCAGTGTCTTTACAGTT 1020
 QY 1283 CTTGTATCCAAATGAAATATCTTAATAGTGGCTCTCTCCCATGAAGAGGATAATCTGAGGAG 1342
 Db 1021 CTTGTATCCAAATGAAATATCTTAATAGTGGCTCTCTCCCATGAAGAGGATAATCTGAGGAG 1080
 QY 1343 ACCGATCATCTGGATATGCTTCTAGTACAGGAACAGATGAACCGCTCTGGAGGAACAC 1402
 Db 1081 ACCGATCATCTGGATATGCTTCTAGTACAGGAACAGATGAACCGCTCTGGAGGAACAT 1140
 QY 1403 GTGCAGTCAACAATGAAGTCTACAGCTGTAAACCATGAAGCAAAATCTGTGGCAGTG 1462
 Db 1141 GTGCAGTCAACAATGAAGTCTACAGCTGTAAACCATGAAGCAAAATCTGTGGCAGTG 1200
 QY 1463 GATGTTATCTCTCATGTNGCAACCCCAACCTTTGAAGAAGACGAACTCTTAATCAAGAG 1522
 Db 1201 GATGTTATCTCTCATGTNGCAACCCCAACCTTTGAAGAAGACGAACTCTTAATCAAGAG 1260
 QY 1523 ACTGCTGTTCCGAGAAATTAATCTTAA 1549
 Db 1261 GCTGCTGTTCCGAGAAATTAATCTTAA 1287

RESULT 13

ABK12991

ID: ABK12991 standard; DNA: 1287 BP.

XX AC ABK12991,

XX DT 23-APR-2002 (first entry)

XX DE Synthetic glioth DNA sequence #5.

XX KW Glioth protein; antiangiogenic; vasotropic; gene therapy;

XX KW dosage form; angiogenesis; neurogenesis; tumour; vascularisation;

XX KW cancer; ischaemia; neuroblastoma; neurodegenerative disease;

XX KW unrecovered nerve trauma; ds.

XX OS Synthetic.

XX PN WO200193681-A1.

XX PD 13-DEC-2001.

XX PF 01-JUN-2001; 2001WO-US18000.

XX PR 02-JUN-2000; 2000US-0586398.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Harland R, Baker JC;

XX DR WPI; 2002-147637/19.

XX PT New compositions comprising glioth proteins, useful for modulating
 angiogenesis or neurogenesis in mammals e.g. for preventing or
 treating undesirable vascularisation of a tumour, ischaemia or
 neurodegenerative disease

XX PS Disclosure, Page 41-42; 45pp; English.

XX CC The present invention relates to a new pharmaceutical composition that
 comprises a glioth polypeptide in dosage form. The glioth polypeptide
 has a sequence identity of at least 75% to the protein sequences
 (AAU74918-AAU74921) fully defined in the specification. The composition
 is useful for modulating angiogenesis or neurogenesis in mammals,
 particularly in humans or mice. Specifically, the composition is useful
 for the prophylactic and/or therapeutic treatment of excess angiogenesis
 e.g. undesirable vascularisation of a tumour or insufficient angiogenesis
 e.g. ischaemia, excess neurogenesis e.g. neuroblastoma or insufficient
 neurogenesis e.g. neurodegenerative disease or unrecovered nerve trauma.

CC The present nucleic acid sequence represents synthetic DNA sequence #5
CC that is one of several artificial goliath nucleic acids (ABK1298-
CC ABK1299) used in the invention for modulating angiogenesis or
CC neurogenesis.

SQ Sequence 1287 BP; 312 A; 321 C; 356 G; 298 T; 0 other;

Query Match 58.88; Score 1042.8; DB 24; Length 1287;
Best Local Similarity 88.1%; Pred. No. 8.7e-280;
Matches 1134; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

[illegible]

RESULT 14

RESOL 14
AAI59292
ID AAI59292 standard: CPNA: 1135 BP

AA59292

XX
XX
XX
XX-XXX-XXXX (first entry)

XX

XX Human; neutropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia; ss.

XX
50
Homo sapiens

XX
PN WO200152312-A1

XX

XX
XXXX
XX

PR 25-APR-2000; 2000US-0552317.

19-JUL-2000 2000US-0620312

PR 03-AUG-2000; 2000US-0633430.
PR 14-SEP-2000; 2000US-0662191

PR 19-OCT-2000; 2000US-0693036.
PR 19-NOV-2000; 2000US-0727344.
PR 19-NOV-2000; 2000US-0727344.

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---	---	---	---	---	---	---	---	---	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	-----

XX

PI Wang J, Wang Z, Wehrman T,

XX
XX

DR P-PSDB: AAM40136.

Novel nucleic acids and poly-

pt
xx
such as central nervous syst

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 31, 2002, 09:55:20, Search time 115 seconds
(without alignments)
5139.275 Million cell updates/sec

Title: US-09-854-300-7

Perfect score: 1774

Sequence: 1 agctggagctccacgcggt....

Scoring table: IDENTITY_NUC ataggcaagttactctctcag 1774

Gapop 10.0, Gapext 1.0

Searched: 310279 seqs, 16457418 residues

Total number of hits satisfying chosen parameters: 620558

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published_Applications_NA:

- 1: /cgn2_6/ptodata/1/pubna/US07_PUBCOMB.seq*
- 2: /cgn2_6/ptodata/1/pubna/PCT_NEW_PUB.seq*
- 3: /cgn2_6/ptodata/1/pubna/US05_NEW_PUB.seq*
- 4: /cgn2_6/ptodata/1/pubna/US06_PUBCOMB.seq*
- 5: /cgn2_6/ptodata/1/pubna/US07_NEW_PUB.seq*
- 6: /cgn2_6/ptodata/1/pubna/PCTNS_PUBCOMB.seq*
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- 9: /cgn2_6/ptodata/1/pubna/US09_NEW_PUB.seq*
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- 11: /cgn2_6/ptodata/1/pubna/US10_NEW_PUB.seq*
- 12: /cgn2_6/ptodata/1/pubna/US10_PUBCOMB.seq*
- 13: /cgn2_6/ptodata/1/pubna/US60_NEW_PUB.seq*
- 14: /cgn2_6/ptodata/1/pubna/US60_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1178.8	66.4	2106	10	US-09-764-864-63
2	1157.6	65.3	1250	10	US-09-764-864-519
3	372.6	21.0	643	9	US-10-046-935-1815
C 4	310	17.5	435	10	US-09-920-300A-1176
C 5	310	17.5	435	12	US-10-031-528-1176
6	274.6	15.5	387	10	US-09-983-965-5551
7	214.4	12.1	374	10	US-09-983-965-4662
8	209	11.8	2063	10	US-09-935-390A-1
9	202.2	11.3	392	10	US-09-983-965-5476
10	187.4	10.6	340	10	US-09-783-590-3523
11	149.2	8.4	1322	10	US-09-935-390A-16
12	132.6	7.5	619	10	US-09-764-864-485
13	117.2	6.6	463	10	US-09-864-761-11364
C 14	112.8	6.4	826	10	US-09-822-849A-90
15	112.4	6.3	435	10	US-09-983-965-5076
16	105.6	6.0	382	10	US-09-815-343-1328
17	105.2	5.9	253	10	US-09-864-761-27944
18	86.4	4.9	922	10	US-09-803-729-23
19	78.8	4.4	570	10	US-09-734-017A-7

C 20	78.6	4.4	439	10	US-09-925-299-484	Sequence 484, App
C 21	77.4	4.4	2244	10	US-09-764-870-222	Sequence 222, App
C 22	76.8	4.3	1355	10	US-09-764-870-182	Sequence 182, App
C 23	76.8	4.3	1355	10	US-09-764-853-404	Sequence 404, App
24	76	4.3	1772	10	US-09-764-853-148	Sequence 148, App
25	75.6	4.3	496	10	US-09-925-301-686	Sequence 686, App
26	75.6	4.3	1906	10	US-09-739-254-32	Sequence 32, Appl
27	75.6	4.3	1906	10	US-09-904-615-32	Sequence 32, Appl
28	75.2	4.2	618	10	US-09-764-853-377	Sequence 377, App
29	75.2	4.2	618	10	US-09-764-898-126	Sequence 126, App
30	75.2	4.2	2330	10	US-04-764-853-184	Sequence 184, App
31	75	4.2	869	10	US-09-764-864-289	Sequence 289, App
32	75	4.2	2751	10	US-09-789-561-64	Sequence 64, Appl
33	75	4.2	2771	10	US-09-925-301-273	Sequence 273, App
34	74.8	4.2	631	10	US-09-908-711-29	Sequence 29, Appl
35	74.8	4.2	640	10	US-09-908-711-28	Sequence 28, Appl
36	74.8	4.2	796	10	US-09-764-853-365	Sequence 365, App
37	74.8	4.2	1454	10	US-09-764-864-91	Sequence 91, Appl
38	74.6	4.2	2005	10	US-09-764-903-22	Sequence 22, Appl
39	74.4	4.2	791	10	US-09-764-853-305	Sequence 305, App
40	74.4	4.2	852	10	US-09-764-898-50	Sequence 50, Appl
C 41	74.4	4.2	852	10	US-09-764-898-123	Sequence 123, App
42	74.4	4.2	1190	10	US-09-410-194-14	Sequence 14, Appl
43	74.4	4.2	1712	10	US-09-925-300-643	Sequence 643, App
C 44	74	4.2	404	10	US-09-969-708-61	Sequence 61, Appl
45	74	4.2	737	10	US-09-764-853-172	Sequence 172, App

ALIGNMENTS

RESULT 1
US-09-764-864-63
Sequence 63, Application US/09764864
Patent No. US6002132753A1
GENERAL INFORMATION:
APPLICANT: Posen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT223
CURRENT APPLICATION NUMBER: US/09/764,864
PRIORITY FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 63
LENGTH: 2306
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-864-63

Query Match	66.4%	Score 1178.8	DB 10	Length 2306
Best Local Similarity	99.0%	Pred. No. 4.9e-294		
Matches 1217	Conservative	0	Mismatches	8
			Indels	4
			Gaps	3
QY	547	CTGTAAACCGCACAGAAATTTACACGGTGTCCACGGTGTGGGAGACACCGGCAAGCTCTC	606	
DB	12	CTGTAAACCGCACAGAAATTTACACGGTGTCCACGGTGTGGGAGACACCGGCAAGCTCTC	71	
QY	607	TTGGTTGGCGCTCATCCACACGCGCGGGGGTGCACCTTCGCACACAGATCCATCTGGC	666	
DB	72	TTGGTTGGCGCTCATCCACACGCGCGGGGGTGCACCTTCGCACACAGATCCATCTGGC	131	
QY	667	TTATAGAGATGAGGAGTGTGGAGAGGAGTATATTTAACTTCGAGGAGGAGGAGGAGTATGAGGT	726	
DB	132	TTATAGAGATGAGGAGGAGTGTGGAGAGGAGTATATTTAACTTCGAGGAGGAGGAGTATGAGGT	191	
QY	727	CATCCCATGTCTCACCGCGGGTGCAGTATGATTTTTCATCATGATGCGCAATCTGAA	786	
DB	192	CATCCCATGTCTCACCGCGGGTGCAGTATGATTTTTCATCATGATGCGCAATCTGAA	251	
QY	787	AGGCAAAAATTCGCAATCTTATCAAGAGGCGATACAGTGCATAGAGT	846	
DB	252	AGGCAAAAATTCGCAATCTTATCAAGAGGCGATACAGTGCATAGAGT	311	

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QY 847 AGGCAAAACATGGGCGCTGGGTGAATCACTATTCAA-TTTTTTCTTTCTGTGTCT 905
Db 312 AGGCAAAACATGGGCGCTGGGTGAATCACTATTCAA-TTTTTTCTTTCTGTGTCT 371
QY 906 TTTTATTATTAAAGGCAAGCACTGTGGGTATTTATCTTTTATCTTTCTGTGTGTAG 965
Db 372 TTTTATTATTAAAGGCAAGCACTGTGGGTATTTATCTTTTATCTTTCTGTGTAG 431
QY 966 GGAATGCAAGAGTCAAGGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1025
Db 432 GGAATGCAAGAGTCAAGGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 491
QY 1026 TTTGAAGGCTTCAACTAGCACTCAAAACAAAGCAAGCAAGCAAGCAAGCAAGCAAG 1085
Db 492 TTTGAAGGCTTCAACTAGCACTCAAAACAAAGCAAGCAAGCAAGCAAGCAAGCAAG 551
QY 1086 ATAGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1145
Db 552 ATAGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 611
QY 1146 GCAACCATATTTTCCATAGACATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1205
Db 612 GCAACCATATTTTCCATAGACATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 671
QY 1206 GCAATGCAAGAGTCAAGGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1265
Db 672 GCAATGCAAGAGTCAAGGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 731
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Db 732 CAGTGTCTTTTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 791
QY 1326 AGGTAATATTAAGGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1385
Db 792 AGGTAATATTAAGGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 851
QY 1386 GGGTCTTTTGGGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1445
Db 852 GGGTCTTTTGGGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 911
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QY 1566 AAGTCTTAATCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1625
Db 1032 AAGTCTTAATCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1091
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Db 1152 ATAGTAAATTTTAAATATTTAAATATTTAAATATTTAAATATTTAAATATTTAAAT 1209
QY 1746 ATATTTTCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1774
Db 1209 ATATTTTCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1237

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RESULT 2

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US-09-764-864-519
; Sequence 519, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

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; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: Patent In Ver 2.0
; SEQ ID NO 519
; LENGTH: 1250
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (540)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1242)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-764-864-519

Query Match 65.3%; Score 1157.6; DB 10; Length 1250;
Best Local Similarity 98.8%; Pred. No. le-288;
Matches 1268; Mismatches 10; Indels 5; Gaps 4;

QY 547 CTCTAAATTAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 606
Db 10 CTCTAAATTAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 77
QY 607 TTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 666
Db 77 TTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 137
QY 726 TTAGAGAGATGAGGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 726
Db 137 TTAGAGAGATGAGGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 197
QY 786 CATCTCCATGTCTCCATCCCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 786
Db 197 CATCTCCATGTCTCCATCCCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 257
QY 846 AGGCACAAAATTTCTGCAATCTATTCAAGAGGCACTACAAGTGCAATGGTGCATAGAAGT 846
Db 257 AGGCACAAAATTTCTGCAATCTATTCAAGAGGCACTACAAGTGCAATGGTGCATAGAAGT 317
QY 905 AGGCAAAACATGGGCGCTGGGTGAATCACTATTCAA-TTTTTTCTTTCTGTGTCT 905
Db 317 AGGCAAAACATGGGCGCTGGGTGAATCACTATTCAA-TTTTTTCTTTCTGTGTCT 377
QY 965 TTTTATTATTAGGCGGCAACTGTGGGCTATTTTATCTTTTATCTGTCTGAAGGCTAC 965
Db 377 TTTTATTATTAGGCGGCAACTGTGGGCTATTTTATCTTTTATCTGTCTGAAGGCTAC 437
QY 1025 GGAATGCAAGAGTCAAGGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1025
Db 437 GGAATGCAAGAGTCAAGGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 497
QY 1084 TTTTGAAGGCTTCAACTAGCACTCAAAACAAAGCAAGCAAGCAAGCAAGCAAGCAAG 1084
Db 497 TTTTGAAGGCTTCAACTAGCACTCAAAACAAAGCAAGCAAGCAAGCAAGCAAGCAAG 557
QY 1144 GATAGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1144
Db 557 GATAGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 617
QY 1209 ATATTTTCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1209
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QY 1264 CCGATGTGTGAATGTCACTACTCAAGGCTTTGGGAATGTAGGTGTGTGTGTGTGTGTGT 1264
Db 677 CCGATGTGTGAATGTCACTACTCAAGGCTTTGGGAATGTAGGTGTGTGTGTGTGTGTGT 737
QY 1324 TCAGTGTCTTTACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1324
Db 737 TCAGTGTCTTTACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 797

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Db 738 TCAGTGTCTTTACAGTCCCTGTATCAATGAATATCTAATAGTGCCTCCTCCCATGAA 797
QY 1325 GAGGATATCGCAGGAGACCGGATCATCTGGATATGCTTCAGTACAGGGAACAGATGAA 1384
Db 798 GAGGATATCGCAGGAGACCGGATCATCTGGATATGCTTCAGTACAGGGAACAGATGAA 857
QY 1385 CCGGCTCTGGAGGAACACGTCGAGTCAACAAATGAAAGTCTACAGTGTGTAACCATGAA 1444
Db 858 CCGGCTCTGGAGGAACACGTCGAGTCAACAAATGAAAGTCTACAGTGTGTAACCATGAA 917
QY 1445 GCAAAATCTGTGGCAGTGGATGTTATTCCTCATGNGAACAACCAACCTTTGAAAGAAC 1504
Db 918 GCAAAATCTGTGGCAGTGGATGTTATTCCTCATGTTGCAACACCAACCTTTGAAAGAAC 977
QY 1505 GAAACTCCTAATCAAGAGACTCTGTGTGAGAAATTAATCTTAAATCTGTGTAATAG 1564
Db 978 GAAACTCCTAATCAAGAGACTCTGTGTGAGAAATTAATCTTAAATCTGTGTAATAG 1037
QY 1565 AAAACTTGAACCTATTAGTAATAACAGAACTGCAACTCAGGCGCTAGTTTCTATTATAAA 1624
Db 1038 AAAACTTGAACCTATTAGTAATAACAGAACTGCAACTCAGGCGCTAGTTTCTATTATAAA 1097
QY 1625 TTGATATAATTAATAAATAAGAGTATGACTGAAAGTCTCAGATGACTAATATATGCG 1684
Db 1098 TTGATATAATTAATAAATAAGAGTATGACTGAAAGTCTCAGATGACTAATATATGCG 1157
QY 1685 TATAGTTAAATGGCTTAAATATTAATTAACCTGTTAACTTTTTCACCAAACTCATAT 1744
Db 1158 TATAGTTAAA--TGGCTTAAATATTAATTAACCTGTTAACTTTTTCACCAAACTCATAT 1214
QY 1745 AATATTTTTCATAGGCAAGTTTC 1767
Db 1215 AATATTTTTCATAGGCAAGTTTC 1237

RESULT 3
US-10-046-935-1815
; Sequence 1815, Application US/10046935
; Patent No. US20020156011A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secrist, Heather
; APPLICANT: Wang, Aijun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.527C1
; CURRENT APPLICATION NUMBER: US/10/046 935
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 2339
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1815
; LENGTH: 643
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: 584
; OTHER INFORMATION: n = A,T,C or G
US-10-046-935-1815

Query Match 21.0%, Score 372.6, DB 2, Length 643,
Best Local Similarity 98.0%; Pred. No. 1.5e-86;
Matches 398; Conservative 0; Mismatches 6; Indels 3; Gaps 2;

QY 1369 ACAGGGAACAGATGAAACCGCTCTGGAGGAACACAGGGAAGTCAACAAATGAAAGTCTACA 1428
Db 1 ACAGGGAACAGATGAAACCGCTCTGGAGGAACACAGGGAAGTCAACAAATGAAAGTCTACA 60
QY 1429 GCTGCTAAACCATGAAGCAAAATCTCTGGCAGTGGATGTTATTCCTCATGTGACAGACCC 1468
Db 61 GCTGCTAAACCATGAAGCAAAATCTCTGGCAGTGGATGTTATTCCTCATGTGACAGACCC 120

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QY 1489 AACCTTTGAAGAGAGAGAAACCTCCTAATCAAGAGACTGCTGTTCGAGAAATTAATCTTA 1548
Db 121 AACCTTTGAAGAGAGAGAAACCTCCTAATCAAGAGACTGCTGTTCGAGAAATTAATCTTA 180
QY 1549 AAATCTGTGTAAATAGAAAACCTTGAACCATTTAGTATTAACAGAACTGCAACTCAGGCGCT 1608
Db 181 AAATCTGTGTAAATAGAAAACCTTGAACCATTTAGTATTAACAGAACTGCAACTCAGGCGCT 240
QY 1609 AGTTTCTATTAAATTAATTTGATAAAATTTAATAAATAAGAGTATGATACTGTAAGTCTCAG 1668
Db 241 AGTTTCTATTAAATTAATTTGATAAAATTTAATAAATAAGAGTATGATACTGTAAGTCTCAG 300
QY 1669 ATGACTAATATTATGCTATAGTTAAATGGCTTAAATAATTTAACTGTTAACTTTTTT 1728
Db 301 ATGACTAATATTATGCTATAGTTAAATGGCTTAAATAATTTAACTGTTAACTTTTTT 358
QY 1729 CCACCAAACTCATTATAATATTTTTCATAGGCAAGTTTCTCTCTCAG 1774
Db 359 CCA-CAAACTCATTATAATATTTTTCATAGGCAAGTTTCTCTCTCAG 403

RESULT 4
US-09-920-300A-1176/c
; Sequence 1176, Application US/09920300A
; Patent No. US30030136728A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.547
; CURRENT APPLICATION NUMBER: US/09/920,300A
; CURRENT FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 1789
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1176
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-920-300A-1176

Query Match 17.5%; Score 310; DB 10; Length 435;
Best Local Similarity 97.4%; Pred. No. 1.7e-70;
Matches 336; Conservative 0; Mismatches 6; Indels 3; Gaps 2;

QY 1430 CTGCTAAACCATGAACCAAAATCTCTGGCAGTGGATGTTATTCCTCATGTGACAGACCA 1489
Db 435 CTGCTAAACCATGAACCAAAATCTCTGGCAGTGGATGTTATTCCTCATGTGACAGACCA 376
QY 1490 ACCTTTCAAGAGAGACCAAACTCCTAATCAAGAGACTGCTGTTCGAGAAATTAATCTTAA 1549
Db 375 ACCTTTGAA-AGAGTGAAG-TCCTAATCAAGAGACTGCTGTTCGAGAAATTAATCTTAA 316
QY 1550 AACTGTGTAATAGAAAACCTTGAACCATTTAGTATTAACAACTGCAACTCAGGCGCTA 1609
Db 315 AACTGTGTAATAGAAAACCTTGAACCATTTAGTATTAACAACTGCAACTCAGGCGCTA 256
QY 1610 GTTCTTATTAAATTTGATGATAAAATTTAATAAATAAGAGTATGATACTGTAAGTCTCAGA 1669
Db 255 GTTCTTATTAAATTTGATGATAAAATTTAATAAATAAGAGTATGATACTGTAAGTCTCAGA 196
QY 1670 TGACTATATATGCTATAGTTAAATTTTAAATTTTAAATTTTAACTGTTAACTTTTTTTC 1729
Db 195 TGACTATATATGCTATAGTTAAA--TGGCTTAAATATTTAACTGTTAACTTTTTTTC 138
QY 1730 CACCAAACTCATTATAATTTTTTTCATAGGCAAGTTTCTCTCTCAG 1774
Db 137 CA-CAAACTCATTATAATTTTTTTCATAGGCAAGTTTCTCTCTCAG 94

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Db 13 CAAGGGCTTCCTCTGGGCAACATCTCGGCGAGCTTAACTGTCGCGGAGTCTTCAAC 72
QY 135 AGCTGGAGCTCC--CAGTCTCACTCCATTCCTTCCCACTCGGCGGCACTGCTCAA 192
Db 73 AGCCGCGGCGGCGGAGTCTGCGGAGTCTGCGGAGTCTTACTATCTGCGGAGTCTGCGG 132
QY 193 GACCAGGCTCTCTCAACCTATAGAGGCGGCGGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGG 252
Db 133 GCGCGGCGGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAG 192
QY 253 GCGCGGCGGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGG 312
Db 193 GCGCGGCGGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGG 252
QY 313 TTCCGAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGG 372
Db 253 TTCCGAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGG 312
QY 373 GCGGCGGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAG 431
Db 313 TGGAGCGGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAG 372
QY 432 GA 433
Db 373 GA 374

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RESULT 8

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US-09-935-390A-1
: Sequence 1, Application US/09935390A
: Patent No. US2002007671A1
: GENERAL INFORMATION:
: APPLICANT: Escobedo, Jaime
: Quianjin, Hu
: Garcia, Pablo
: Williams, Lewis T.
: Kothakota, Srinivas
: NUMBER OF INVENTION: Secreted Human Proteins
: NUMBER OF SEQUENCES: 38
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Chiron Corporation
: STREET: 4560 Horton Street
: CITY: Emeryville
: STATE: CA
: COUNTRY: USA
: ZIP: 94608-2916
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/935,390A
: FILING DATE: 22-Aug-2001
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/988,671
: FILING DATE: 1997-12-11
: ATTORNEY/AGENT INFORMATION:
: NAME: Jane E. R. Potter
: REGISTRATION NUMBER: 33,332
: REFERENCE/POCKET NUMBER: 1364 002
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (510) 923-2718
: TELEFAX: (510) 655-3542
: TELEX: <unknown>
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2063 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear

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FEATURE:

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: SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-935-390A-1

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Query Match 11.8% Score 209; DB 10; Length 2063;
Best Local Similarity 54.6% Pred. No. 4.4e-44;
Matches 507; Conservative 0; Mismatches 410; Indels 12; Gaps 4;

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QY 339 TCGTGGGCTCTAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGG 198
Db 180 TCGTGGGCTCTAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGG 239
QY 359 ACCTCAACGTTGCTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGG 458
Db 240 CCCT---GGTAAACATCGAGTACGTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGG 296
QY 459 GCGAGGAGGCGGTGTACGGCCAGGACTCGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGG 518
Db 297 GCGAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGG 356
QY 519 GCGCGGAGGCGGCGGCGGCGGCTTAAACGCGCTGTAAACGCGCTGTAAACGCGCTGTAAACGCGCT 578
Db 357 TCCGCTGCGGCGGCGGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAG 416
QY 579 CGGTTTGGGGAAGCACCGTGTCAAGTCTCTTGGTTGGCGCTCATCCCAACGCGGCGGCGGCT 638
Db 417 CCGAGCGCGGCGGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGG 473
QY 639 GCACCTTGGCGAGACAGATCCATCTGGCTTATGAGAGATGGGCGTCTGCGGAGTCTGCGGAGTCTGCGG 698
Db 474 GCACCTTCAAGAGCAAGTGTGCTGGCGGCGGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGG 533
QY 659 TTAACCTCCCGGCGGCGGCGGCAATGAGGTCTATCCCATCTCTACCGCGGCGGCGGAGTCTGCGGAG 758
Db 534 ACATGAGGAGGCGGTACGGGAAATCATCACTTTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGG 593
QY 759 TTGTTGCAATCATCTGCGCAATCTGAAAGGCGACAAATTTGCAATCTATTTCAAGAG 818
Db 594 TAGTGGTCTATTGATTAGTATCTCAAAAGGAGAGAAATTTGGAGCTGGTCAAAAG 853
QY 819 GCATACAGTGCACATGCTCATAGAGTGGGAAAGAACATGCGCCCTTGGTCAATCAC- 877
Db 654 GAATTCAGTAACGATGACCAIAGGGGTTGGCGGCGGCGGAGTCTGCGGAGTCTGCGGAGTCTGCGGAG 713
QY 878 --TATTCAATTTTTTCTGCTGCTCTTTTATTATTATAGGCGGCGGCAACTGTGGGCT 935
Db 714 GTCAGTCTGTGTGTTGTTGGCGCTTCTCATCACTGATGATTATCTCGTTAGCCT 773
QY 936 AITTTATCTTTTATCTGCTGCGGAGGCTACGGAATCAAGAGTCAAAAGGAGAGACAGA 995
Db 774 GCGTAATATTTTACTATATACAGGCTTCTCTATATATCTGCTCTCAGATTGGAAGTCAGA 833
QY 996 GCGTAATTAAGGCGAGTCTTAAAGAGCTATTGAGGCTTCAACTACGACACTCAAGC 1055
Db 834 GCCATAGAAA--AGAACTAAGAAAGTTATTGGCCAGCTTCTACTTCTATCATCTGTAAGC 890
QY 1056 AAGGAGCAAGGAAATTTGGCGCTGATGAGATAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1115
Db 891 ATGGAGAAAGGAAATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 950
QY 1116 AACCAATGATTTGGTACGATCTTACGTCGCAACCATATTTTCCATAGACATGTTG 1175
Db 951 AAGTAAGGATATTATTAGATTTCTGCCATGCAAGCATATTTTTCATAGATATGATTG 1010
QY 1176 ACCATGCTCTTAAACACAGACTTGGCGGCTTGGCGGCTTGGCGGCTTGGCGGCTTGGCGGCTTGGCGG 1235
Db 1011 ACCATGCTCTTAAACACAGACTTGGCGGCTTGGCGGCTTGGCGGCTTGGCGGCTTGGCGGCTTGGCGG 1070
QY 1236 TGGGAATGAGTGGGATGTTGAAGATGA 1264
Db 1071 TAGGATATTGGGAGAGCCTGGGATGTA 1099

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RESULT 9
 US-09-983-965-5467
 : Sequence 5467, Application US/09983965
 : Patent No. US20020137160A1
 : GENERAL INFORMATION:
 : APPLICANT: Warren, Wesley C.
 : APPLICANT: Tao, Nengbing
 : APPLICANT: Wyatt, John C.
 : APPLICANT: Mathialagan, Nagappan
 : TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
 : : TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
 : FILE REFERENCE: 37-21(10297)C
 : CURRENT APPLICATION NUMBER: US/09/983,965
 : PRIOR FILING DATE: 2001-10-26
 : PRIOR APPLICATION NUMBER: US 06/465,231
 : PRIOR FILING DATE: 1999-12-15
 : PRIOR APPLICATION NUMBER: US 60/113,678
 : PRIOR FILING DATE: 1998-12-17
 : NUMBER OF SEQ ID NOS: 5912
 : SEQ ID NO 5467
 : LENGTH: 392
 : TYPE: DNA
 : ORGANISM: Bos taurus
 : FEATURE:
 : OTHER INFORMATION: Clone ID: 46-LIR44-036-Q1-F1-D10
 US-09-983-965-5467

Query Match 11.3% Score 201.2; DB 10; Length 392;
 Best Local Similarity 80.3%; Pred. No. 1.7e-42;
 Matches 285; Conservative 0; Mismatches 64; Indels 6; Gaps 4.

QY 1418 GAAAGCTACAGCTGGTAAACATGAGCAAAATTCCTGGCAGTGGATGTTATTCCTCAT 1477
 DB 1 GAAATCTACAGCTGGTAAACATGAGCAAAATTCCTGGCAGTGGATGTTATTCCTCAC 60
 QY 1478 GTNACACCTAACTTTGAGAGAGAGCAAACTCTTAATTAAGAGACTGTGTTCGAGAA 1537
 DB 61 GTGACAACTAACTTTGAGAGAGAGCAAACTCTTAATTAAGAGACTGTGTTCGAGAA 119
 QY 1538 ATTAATCTTAAATCTGTGTAAATAGAAACTTGAACACTTAGTAAATAGCAAACTGCC 1597
 DB 120 ATTAATCATAAATCCGTATCANTTGAARAACCTGACCTTTAATAATACAAACCTGCC 179
 QY 1598 AATC-AGGCGCTATTTCTATTATAAATGCGATAAATTTAATAAATAAGAGAGTACT 1656
 DB 180 AATTAAGGCGCAATTTACAAATAAGGGAATGGTAAACCTTTAATAATATCAAGAGACT 239
 QY 1657 GAAAGTGTGAGAGCACTAATATTATGCTATAGTTAAATGCGCTTAAATATTTAACT 1716
 DB 240 GAAATGTGATATGACTTAATATTATG-TATATTAAT--TGAATTAATATCAAACT 297
 QY 1717 GTTAACCTTTTCCACCAACTCATTATATATTTTTCATAGGCAAGTTTCCCTCT 1771
 DB 298 ATTAACCTTTT--CCACAACACATTATATAAGTTTTCATAGGCAAAATTTCCCTCT 350

RESULT 10
 US-09-783-590-3523
 : Sequence 3523, Application US/09783590
 : Patent No. US20020110850A1
 : GENERAL INFORMATION:
 : APPLICANT: Dillion, Patrick J.
 : APPLICANT: Haseltine, William A.
 : APPLICANT: Li, Haodong
 : APPLICANT: Rosen, Craig A.
 : APPLICANT: Ruben, Steven M.
 : TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
 : FILE REFERENCE: PO-16.2C1
 : CURRENT APPLICATION NUMBER: US/09/783,590
 : CURRENT FILING DATE: 2000-02-15
 : PRIOR APPLICATION NUMBER: 08/420,856
 : PRIOR FILING DATE: 1995-04-12
 : PRIOR APPLICATION NUMBER: 08/346,741

: PRIOR FILING DATE: 1994-11-21
 : NUMBER OF SEQ ID NOS: 12485
 : SOFTWARE: PatentIn Ver. 2.0
 : SEQ ID NO 3523
 : LENGTH: 340
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : FEATURE:
 : NAME/KEY: misc feature
 : LOCATION: (205)
 : OTHER INFORMATION: n equals a,t,g, or c
 : NAME/KEY: misc feature
 : LOCATION: (320)
 : OTHER INFORMATION: n equals a,t,g, or c
 : NAME/KEY: misc feature
 : LOCATION: (221)
 : OTHER INFORMATION: n equals a,t,g, or c
 : NAME/KEY: misc feature
 : LOCATION: (244)
 : OTHER INFORMATION: n equals a,t,g, or c
 : NAME/KEY: misc feature
 : LOCATION: (265)
 : OTHER INFORMATION: n equals a,t,g, or c
 : NAME/KEY: misc feature
 : LOCATION: (294)
 : OTHER INFORMATION: n equals a,t,g, or c
 : NAME/KEY: misc feature
 : LOCATION: (318)
 : OTHER INFORMATION: n equals a,t,g, or c
 : NAME/KEY: misc feature
 : LOCATION: (333)
 : OTHER INFORMATION: n equals a,t,g, or c
 US-09-783-590-3523

Query Match 10.6% Score 187.4; DB 10; Length 340;
 Best Local Similarity 97.0%; Pred. No. 5.8e-39;
 Matches 191; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1203 GCGCATGTGCGCAAAATGTCACATACCTCAAAAGCTTTGGGAATTGAGTGGATGTTGAAGATG 1262
 DB 1 GCGCATGTGCGCAAAATGTCACATACCTCAAAAGCTTTGGGAATTGAGTGGATGTTGAAGATG 60
 QY 1263 GATCAGTGTCTTTACAAAGTCCCTGTATCCAAATCAATATCTATATAGTCCCTCCTCCATG 1322
 DB 61 GATCAGTGTCTTTACAAAGTCCCTGTATCCAAATCAATATCTATATAGTCCCTCCTCCATG 120
 QY 1323 AAGAGGATATGCGAGTGGAGAGCGGATCATCTGATATCTTCAGTACAGGAACAGATG 1382
 DB 121 AAGAGGATATGCGAGTGGAGAGCGGATCATCTGATATCTTCAGTACAGGAACAGATG 180
 QY 1383 AACCGCTCTCTGGAGGAA 1399
 DB 181 AACCGCTCTCTGGAGGTA 197

RESULT 11
 US-09-935-390A-16
 : Sequence 16, Application US/09935390A
 : Patent No. US20020076761A1
 : GENERAL INFORMATION:
 : APPLICANT: Escobedo, Jaime
 : : Quijano, Hu
 : : Garcia, Pablo
 : : Williams, Lewis T.
 : : Kothakota, Srinivas
 : TITLE OF INVENTION: Secreted Human Proteins
 : NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Chiron Corporation
 STREET: 4560 Horton Street
 CITY: Emeryville
 STATE: CA
 COUNTRY: USA
 ZIP: 94608-2916
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/935,390A
 FILING DATE: 22-Aug-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/988,671
 FILING DATE: 1997-12-11
 ATTORNEY/AGENT INFORMATION:
 NAME: Jane E. R. Potter
 REGISTRATION NUMBER: 33,332
 REFERENCE/DOCKET NUMBER: 1369,002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (510) 923-2718
 TELEFAX: (510) 655-3542
 TELEX: <Unknown>
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1322 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 16:
 US-09-935-390A-16

Query Match 8.4%; Score 149.2; DB 10; Length 1322;
 Best Local Similarity 56.1%; Pred. No. 8.4e-29;
 Matches 302; Conservative 0; Mismatches 233; Indels 3; Gaps 1;

QY 720 ATGAGGTCATCCCATCTCTACCGGGTGCAGTACACATTTGTCGAATCATGATCGGCA 779
 Db 259 AGGAGCAGTTACCATGACTACCTCCAGGACTGGAGATATATTGCTGATGATAACAG 318
 QY 780 ATCTGAAGGACACAAAATCTGCAATCTATTCAAAGAGGACATACAAAGTACAAATGGTCA 839
 Db 319 AATTGAGGGTGAAGATATTTGAGTTATCTGGAGAAACATCTCTGTACAAATGACAA 378
 QY 840 TAGAAGTAGGMAAACATGGCCCTTGGG---TGAATCACTATTCAATTTTTCGGTT 896
 Db 379 TAGCTGTGGAACTCGAATGCGACCGGAAGAACTTCAGCGGTGGCTCTCTAGCTTCGGT 438
 QY 897 CTGTGCTCTTTTATTATTACGGGGAACCTGTGGCTATTATTATCTTTTATCTGCT 956
 Db 439 CAATATCTTTTATTTTGTATGATATTTTCTTCAGCATGGCTCATATTTCTACTTCATTC 498
 QY 957 GAAGGCTACGAATGCAAGAGCTCAAGAGCAGGAGGCAATTTAAAGGAGAGATGCTA 1016
 Db 499 AAAAGATCAGGTACACAAATGCAGCGACAGCAAGCAAGGCTGCTCTCGGAGATGCGCA 558
 QY 1017 AAAAGCTATTGGAGGCTTCACTAGGCACATGAAACAGGACAGGAAATTTGGCC 1076
 Db 559 AGAAGGCATCAGTAATTTACAAACCCAGGACACTAAGAGGGGTGACAGGAAATTCAC 618
 QY 1077 CTGATGGAGATAGTTGTGTGTGTGATTCGAATTTGAACCAAAATGATTTGGTACGCA 1136
 Db 619 CAGACTTTGATCTGTGCTAGCTCTGATAGAGAGCTATAGCAGAAATGATGTCGTCGAA 678
 QY 1137 TCTTAAGCTGCAACATATTTTCCATAAGACATGTGTGACCAATGAGTGTGTTAAACATA 1196
 Db 679 TCTCCCTTCAGCAATTTTTCACAAATGCGGTGAGATGCTGCTTACTGTAACATT 738
 QY 1197 AGACTGCCCATGTGCAAAATGTGACATACCTTAAATTTTGCGGAATTTGAGTGTGAT 1254

Db 739 GTACCTGCTGATGTAACACTTAATATATTAAGGCTCTCTGGGAATTTGTGCGCAATTT 796
 RESULT 12
 US-09-764-864-485
 : Sequence 485, Application US/09764864
 : Patent No. US20020132753A1
 : GENERAL INFORMATION:
 : APPLICANT: Rosen et al.
 : TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 : FILE REFERENCE: PT223
 : CURRENT APPLICATION NUMBER: US/09/764,864
 : CURRENT FILING DATE: 2001-01-17
 : Prior application data removed - consult PALM or file wrapper
 : NUMBER OF SEQ ID NOS: 1792
 : SOFTWARE: Patent In Ver. 2.0
 : SEQ ID NO 485
 : LENGTH: 619
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : US-09-764-864-485

Query Match 7.5%; Score 132.6; DB 10; Length 619;
 Best Local Similarity 60.3%; Pred. No. 1.1e-24;
 Matches 219; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

QY 869 GTGAATCACTATTCAATTTTTCGTTTCGTCTGCTCTTTTATTTATTTACGGCGGCAACT 928
 Db 32 GTGAGCGGCACCTTCGGTTGTTGCTGCTCATCTCCTTCATTTGCTGATGATCATTTCC 91
 QY 929 GTGAGCTATTATTATCTTTTATTCTCTCGAAGGCTACGGAATGCAAGAGCTCAAGCAGG 988
 Db 92 CTCGATGGCTGCTCTTTTATTACATCCAGAGGTTTCGATATGCAATGCCAGGATAGG 151
 QY 989 AAGCAGAGGCAATTAAGGCGAGATGCTAAAAAGCTATTGGAAGGCTTCAACTACGCACA 1048
 Db 152 AACCCAGCGGACTGGGGATGACGCAAGAAAGCAATCAGCAAACTCCAGATCAGGACC 211
 QY 1049 CTGAACAAGGACAGACAGGAATTTGGCCCTGATGGAGATAGTTGCTCTGTGCTGCTGAA 1108
 Db 212 ATCAAGAAGGCTGACAGGAACAGAGTCTGATTTTGACAACTGTGCACTTTGTATTTGAA 271
 QY 1109 TTGTATAAACAATGATTTGGTACGCATCTTAACGTGCAACCATATTTTCCATAGACA 1168
 Db 272 GGGTACAGCCCAATGACGTTGTCGGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 331
 QY 1169 TGTGTTGACCATGCGCTGTTTAAACACACAACTTTGCGGCTATGTCGCTGCTGCTGCTGCT 1228
 Db 332 TGTGTTGACCGCTGCTTCTAGACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 391
 QY 1229 AAA 1231
 Db 392 AAA 394

RESULT 13
 US-09-864-761-11364
 : Sequence 11364, Application US/09864761
 : Patent No. US20020048763A1
 : GENERAL INFORMATION:
 : APPLICANT: Penn, Sharon G.
 : APPLICANT: Panv, David P.
 : APPLICANT: Hanzel, David K.
 : APPLICANT: Chen, Wensheng
 : TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
 : FILE REFERENCE: Aeonica-X-1
 : SUPPLEMENT APPLICATION NUMBER: US/09/864,761
 : CURRENT FILING DATE: 2001-05-23
 : PRIOR APPLICATION NUMBER: US 60/180,312
 : PRIOR FILING DATE: 2000-02-04
 : PTO/P APPLICATION NUMBER: US 66/207,456


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: FILE REFERENCE: 37-21(10297)C
: CURRENT APPLICATION NUMBER: US/09/983,965
: CURRENT FILING DATE: 2001-10-26
: PRIOR APPLICATION NUMBER: US 09/465,231
: PRIOR FILING DATE: 1999-12-15
: PRIOR APPLICATION NUMBER: US 66/113,678
: PRIOR FILING DATE: 1998-12-17
: NUMBER OF SEQ ID NOS: 5912
: SEQ ID NO 5079
: LENGTH: 435
: TYPE: DNA
: ORGANISM: Bos taurus
: FEATURE:
: OTHER INFORMATION: Clone ID: 31-LIB34-050-Q1-E1-H3
US-09-983-965-5079

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Query Match      6.3%   Score 112.4; DB 10; Length 435;
Best Local Similarity 86.0%; Pred No 1.4e-19;
Matches 160; Conservative 0; Mismatches 21; Indels 5; Gaps 3;

QY 1587 ACAGAACTGCCAATCAGGCGCTAGTTT-CIATTATAAATTCGATAAAATTTAATAAAATA 1645
DB 1 ACAGAACTGCCAATCAGGCGCTAGTTTACCTAGTAAGGAACTGSAIAAAATTAAIAAAATA 50

QY 1646 AGAGTGATATGSAAGTGTACATGACTAATATATGCTATAGTTAAATGCTTAAAAA 1705
DB 61 AGAATGATATGSAAGTGTATGATGACTAATAATATATGCTATAGTTAAA--TGACTTAAA 118

QY 1706 ATATTTAAGCTTTAAGTTTTTTCCACCAACATCATTATAATATTTTCATAGGCAAGTT 1765
DB 119 ATACTAAACCTATTAACTTTT--CCACAAATACATTATAATGTTTTTCATAGGCAAGTT 176

QY 1766 TCCCTCT 1771
DB 177 TCCCTCT 182

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Job time : 128 secs

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 31, 2002 08:33:05 : Search time 60 seconds
(without alignments)
6326 100 Million cell updates/sec

Title: US-09-854-300-7

Perfect score: 1774

Sequence: 1 agctgagctccacgcggt atagggaagtttctcttcag 1774

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 20000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2_6/ptodata/1/ina/6A_COMB seq *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	147.6	8.3	1253	2	US-08-786-606-6
2	77	4.3	912	2	US-09-090-567-3
3	76.4	4.3	2605	2	US-08-680-375-4
4	73.8	4.2	1378	1	US-08-075-533-20
5	73.8	4.2	1378	2	US-08-948-176-20
6	73.8	4.2	1378	5	PCT-US91-09160-20
7	73.8	4.2	1556	4	US-09-043-937A-1
8	73.8	4.2	1568	4	US-09-043-937A-1
9	73.2	4.1	1543	4	US-09-227-357-25
10	73	4.1	1545	4	US-09-227-357-125
11	73	4.1	1585	4	US-09-183-861-54
12	73	4.1	1585	4	US-09-022-765-64
13	73	4.1	2775	1	US-08-730-771-1
14	73	4.1	2775	4	US-09-060-208-1
15	73	4.1	3089	1	US-08-472-934-5
16	73	4.1	3089	2	US-08-323-460A-5
17	73	4.1	3089	4	US-08-461-145C-5
18	73	4.1	3089	3	US-08-461-145C-5
19	73	4.1	3089	4	US-08-628-829-9
20	73	4.1	3328	4	US-08-960-048-1
21	71.4	4.0	2045	4	US-08-795-088A-1
22	71	4.0	625	4	US-09-288-143-17
23	70.4	4.0	2085	2	US-08-668-1288-7
24	70.4	4.0	2085	2	US-08-905-445-7
25	69.4	3.9	633	4	US-08-818-112-6
26	69.4	3.9	633	4	US-08-818-111-6
27	69.4	3.9	633	4	US-09-056-556-6

Sequence 6, Appli
Sequence 101, App
Sequence 96, Appl
Sequence 101, App
Sequence 96, Appl
Sequence 1, Appli
Sequence 107, App
Sequence 4, Appli
Sequence 108, App
Sequence 14, Appl
Sequence 5, Appli
Sequence 9, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 1, Appli
Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-786-606-6
: Sequence 6, Application US/08786606
: Patent No. 5861495
: GENERAL INFORMATION:
: APPLICANT: Hillman, Jennifer L.
: APPLICANT: Au-Young, Janice
: APPLICANT: Coleman, Roger
: APPLICANT: Goli, Surya K.
: TITLE OF INVENTION: NOVEL HUMAN ZINC-BINDING
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Incyte Pharmaceuticals, Inc.
: STREET: 3174 Porter Drive
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94304
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US-08/786,606
: FILING DATE:
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Billings, Lucy RJ
: REGISTRATION NUMBER: 36,749
: REFERENCE/AGENT NUMBER: PP-0173 US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-855-0555
: TELEFAX: 415-845-4166
: TELEX:
: INFORMATION FOR SEQ ID NO. 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1253 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
US-08-786-606-6

Query Match 8.3% Score 147.6; DB 2: Length 1253;
Best Local Similarity 55.9%; Pred. No. 2.6e-31;
Matches 301; Conservative 0; Mismatches 234; Indels 3; Gaps 1;

QY 720 ATGAGTCATCCGATGTCATCCGCGGCTGAGTACATATTGTTGTAATCATGATGAGCA 779
Db 242 AGAGAGCAGTATGACATGACTATCCAGGACCTGGAGATATTATGCTGCTCAATGAAAG 301
QY 780 ATGTAAGAGGACAAATATTCATATTAATTAAGATGATATAAATGACATGATGCA 839
Db 302 AATTGAGGCTAAGATATTTAGTTATTTGAGAGAAATATCTCTGTACAAATGACAA 361
QY 840 TAGAAGTAGGAAACATGAGGCTTGGG---TGAATCACTATTCATATTTTTCGTT 896
Db 362 TAGCTGTGTAATGGAATGATGATGAGAGAAATTCAGGATGATGATGATGATGAT 421
QY 897 CTGCTGCTGTTTTTATTAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 955
Db 422 CAATATGCTTATGTTGATGATATTTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAG 481
QY 957 GAAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1016
Db 482 AGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 541
QY 1017 AAAAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1076
Db 542 AGAAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 601
QY 1077 CTGATGAGGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1136
Db 602 CAGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 661
QY 1137 TTTTAAAGTGAAGTATATTTTGAAGTATGATGATGATGATGATGATGATGATGATGAT 1196
Db 662 TTTTAAAGTGAAGTATATTTTGAAGTATGATGATGATGATGATGATGATGATGATGAT 721
QY 1197 AGATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1254
Db 722 GTATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 779

RESULT 2
US-09-090-567-3
Sequence 3, Application US/09090567
Patent No. 598540
GENERAL INFORMATION:
APPLICANT: Sullivan, Robert
APPLICANT: Brub, Bruno
APPLICANT: Lgar, Christine
APPLICANT: Gaudreault, Christian
TITLE OF INVENTION: Acrosomal Sperm Protein And
TITLE OF INVENTION: Uses Thereof
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swabey Ogilvy Penault
STREET: 1600 - 1981 McGill College
CITY: Montreal
STATE: QC
COUNTRY: Canada
ZIP: H3A 2Y3
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/090,567
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Murphy, Kevin P
REGISTRATION NUMBER: 26,674
REFERENCE/DOCKET NUMBER: 13045-2"US" PC/PC

TELECOMMUNICATION INFORMATION:
TELEPHONE: 514-845-7126
TELEFAX: 514-288-8389
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 912 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
US-09-090-567-3

Query Match 4.3%; Score 77; DB 2; Length 912;
Best Local Similarity 94.1%; Pred. No. 1.1e-11;

Matches 80; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AGCTGGAGTCCACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
Db 7 AGCTGGAGTCCACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 66
QY 61 AATTCGGACGAGCCGAGGAGGCTGC 85
Db 67 AATTCGGACGAGCCGAGGAGGCTGC 91

RESULT 3
US-08-680-395-4
Sequence 4, Application US/08680395
Patent No. 5892010
GENERAL INFORMATION:
APPLICANT: Gray, Joe W.
APPLICANT: Collins, Colin
APPLICANT: Hwang, Soo in
APPLICANT: Godfrey, Tony
APPLICANT: Kowbel, David
APPLICANT: Rommens, Johanna
TITLE OF INVENTION: Genes from the 20q13 Amplicon and Their
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/680,395
FILING DATE: 15-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 021070-06890005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2605 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: -

LOCATION: 1, 2605
 OTHER INFORMATION: Zeta-2 DNA clone 0.43 of 4 kb
 OTHER INFORMATION: transcript
 US-08-680-348-4

Query Match 4.3%; Score 76.4; DB 2; Length 2605;
 Best Local Similarity 80.9%; Pred. No. 2, 8e-11;
 Matches 89; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 AGCTGGAGTTCACGGGCTGGGGGCTGGGCTGTAGAACTAGTATGATGCTGGGGCTGGAGG 60
 DB 36 AGCTGGAGTTCACGGGCTGGGGGCTGGGCTGTAGAACTAGTATGATGCTGGGGCTGGAGG 95
 QY 61 AATTCGGACGAGGAGGAGTATCTATCTGGGCAATCTGTGTGTAGG 110
 DB 96 AATTCGGACGAGGAGGAGTATCTATCTGGGCAATCTGTGTGTAGG 145

RESULT 4
 US-08-075-533-20
 : Sequence 20, Application US/08075533
 : Patent No. 5530186
 : GENERAL INFORMATION:
 : APPLICANT: Hitz, William D.
 : TITLE OF INVENTION: Nucleotide Sequences of Soybean Acyl-ACP
 : TITLE OF INVENTION: Thioesterase Genes
 : NUMBER OF SEQUENCES: 22
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: E I du Pont de Nemours and Company
 : STREET: 1007 Market Street
 : CITY: Wilmington
 : STATE: Delaware
 : COUNTRY: U.S.A.
 : ZIP: 19898
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent In Release #1 0, Version #1 25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/075,533
 : FILING DATE:
 : CLASSIFICATION: 800
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 07/631,264
 : FILING DATE: 20-DEC-1990
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Morrissey, Bruce W.
 : REGISTRATION NUMBER: 30,663
 : REFERENCE/DOCKET NUMBER: CP-8026-A
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (302) 992-4927
 : TELEX: (302) 892-7949
 : INFORMATION FOR SEQ ID NO: 20:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 1378 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: DNA (genomic)
 : ORIGINAL SOURCE:
 : ORGANISM: Brassica napus
 : US-08-075-533-20

Query Match 4.2%; Score 73.8; DB 1; Length 1378;
 Best Local Similarity 97.4%; Pred. No. 1, 1e-10;
 Matches 75; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGCTGGAGTTCACGGGCTGGGGGCTGGGCTGTAGAACTAGTATGATGCTGGGGCTGGAGG 60
 DB 52 AGCTGGAGTTCACGGGCTGGGGGCTGGGCTGTAGAACTAGTATGATGCTGGGGCTGGAGG 111

QY 61 AATTCGGACGAGGAGGAGTATCTATCTGGGCAATCTGTGTGTAGG 77
 DB 112 AATTCGGACGAGGAGGAGTATCTATCTGGGCAATCTGTGTGTAGG 128

RESULT 5
 US-08-948-176-20
 : Sequence 20, Application US/08948176
 : Patent No. 5945585
 : GENERAL INFORMATION:
 : APPLICANT: Hitz, William D.
 : TITLE OF INVENTION: Acyl-ACP Thioesterase Genes
 : TITLE OF INVENTION: AND THEIR USE IN ALTERING PLANT
 : TITLE OF INVENTION: OIL COMPOSITION
 : NUMBER OF SEQUENCES: 26
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: E I du Pont de Nemours and Company
 : STREET: 1007 Market Street
 : CITY: Wilmington
 : STATE: Delaware
 : COUNTRY: UNITED STATES OF AMERICA
 : ZIP: 19898
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: DISKETTE, 3.50 INCH
 : COMPUTER: IBM PC COMPATIBLE
 : OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
 : SOFTWARE: MICROSOFT WORD VERSION 7.0
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/948,176
 : FILING DATE:
 : CLASSIFICATION: 800
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 07/631,264
 : FILING DATE: DECEMBER 20, 1990
 : ATTORNEY/AGENT INFORMATION:
 : NAME: CHRISTENBURY, LYNNE M.
 : REGISTRATION NUMBER: 30,971
 : REFERENCE/DOCKET NUMBER: CP-8426-C
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 302-992-5481
 : TELEX: 302-773-0164
 : INFORMATION FOR SEQ ID NO: 20:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 1378 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: DNA (genomic)
 : ORIGINAL SOURCE:
 : ORGANISM: Brassica napus
 : US-08-948-176-20

Query Match 4.2%; Score 73.8; DB 2; Length 1378;
 Best Local Similarity 97.4%; Pred. No. 1, 1e-10;
 Matches 75; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGCTGGAGTTCACGGGCTGGGGGCTGGGCTGTAGAACTAGTATGATGCTGGGGCTGGAGG 60
 DB 52 AGCTGGAGTTCACGGGCTGGGGGCTGGGCTGTAGAACTAGTATGATGCTGGGGCTGGAGG 111
 QY 61 AATTCGGACGAGGAGGAGTATCTATCTGGGCAATCTGTGTGTAGG 77
 DB 112 AATTCGGACGAGGAGGAGTATCTATCTGGGCAATCTGTGTGTAGG 128

RESULT 6
 PCT-US91-09160-20
 : Sequence 20, Application PCT/US9109160
 : GENERAL INFORMATION:
 : APPLICANT: Hitz, William D.
 : APPLICANT: Yadav, Narendra S.

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0. Version #1.10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/043,937A
FILING DATE: 24-Jul-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FW96/01544
FILING DATE: 03-OCT-1996
APPLICATION NUMBER: FR 95,11623
FILING DATE: 03-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 1487-20
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1568 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: cDS
LOCATION: 278..1306
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-043-937A-1

Query Match 4.28; Score 73.8; DB 4; Length 1568;
Best Local Similarity 97.4%; Pred. No. 1.1e-10;
Matches 75; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 AGCTGGAGCTCCACCGCGTGGGCGGCTCTAGAACTAGTGGATCCCGGGCGTCGAGG 60
|||||
Db 47 AGCTGGAGCTCCACCGCGTGGGCGGCTCTAGAACTAGTGGATCCCGGGCGTCGAGG 105
QY 61 AATTCGGCAGGAGCCGA 77
|||||
Db 107 AATTCGGCAGGAGGGA 123

RESULT 9

US-09-227-357-26
Sequence 26, Application US-09-227-357
Patent No. 6342581
GENERAL INFORMATION:
APPLICANT: Fischer et al.
TITLE OF INVENTION: 123 Human Secreted Proteins
FILE REFERENCE: P2010P1
CURRENT APPLICATION NUMBER: US/09/227,357
CURRENT FILING DATE: 1999-01-08
EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: 60/051,926
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,793
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,925
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,924
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,803
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,732
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,931
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,932

EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,916
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,930
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,918
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,920
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,733
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,795
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,919
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,928
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/055,722
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,723
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,948
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,949
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,953
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,950
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,947
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,964
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/056,360
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,684
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,984
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,954
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/058,785
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,664
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,660
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,661
EARLIER FILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 672
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 26
LENGTH: 1543
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (69)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (717)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (899)
OTHER INFORMATION: n equals a,t,g, or c
US-09-227-357-26

Query Match 4.18; Score 73.2; DB 4; Length 1543;
Best Local Similarity 73.8%; Pred. No. 1.7e-10;
Matches 93; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/183.861
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/022.765
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420C3
TELEPHONE: (206) 622-4900
TELEFAX: (206) 622-4900
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 1585 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-183-861-54

Query Match 4.1% Score 73 DB 4: Length 1585;

Best Local Similarity 100.0% Pred No. 1 9e-10; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGTCTCCACGGCGGTGGCGGCGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 60
|||||
DB 3 AGCTGAGTCTCCACGGCGGTGGCGGCGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 62

QY 61 AATTGGGCACGAG 74
|||||
DB 63 AATTGGGCACGAG 75

RESULT 12

US-09-022-765-54

Sequence 54, Application US/09/022.765
Patent No. 6375955

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Campos-Neto, Antonio

APPLICANT: Webb, John R.

APPLICANT: Dillon, David C.

APPLICANT: Skeiky, Yasir A. W.

TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE THERAPY AND

NUMBER OF SEQUENCES: 87

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/022.765

FILING DATE: 12-FEB-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420C3
TELEPHONE: (206) 622-4900
TELEFAX: (206) 622-4900
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 1585 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-022-765-54

Query Match

Best Local Similarity 100.0% Pred No. 1 9e-10;

Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGTCTCCACGGCGGTGGCGGCGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 60
|||||
DB 3 AGCTGAGTCTCCACGGCGGTGGCGGCGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 62

QY 61 AATTGGGCACGAG 73
|||||
DB 63 AATTGGGCACGAG 75

RESULT 13

US-08-730-771-1

Sequence 1, Application US/08730771

Patent No. 5780609

GENERAL INFORMATION:

APPLICANT: Marshall, Lisa

APPLICANT: Roshak, Amy

TITLE OF INVENTION: A NOVEL HUMAN B-CELL SURFACE MOLECULE

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporation

STREET: 700 Swedeland Road

CITY: King of Prussia

STATE: PA

COUNTRY: USA

ZIP: 19406-2799

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/730.771

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Han, William T

REGISTRATION NUMBER: 34,344

REFERENCE/DOCKET NUMBER: P50380

TELEPHONE: 610-270-5219

TELEFAX: 610-270-5090

TELEX:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2775 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-730-771-1

Query Match 4.1%; Score 73; DB 1; Length 2775;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGCTCCACCGGCTGGCGGCGCTCTAGAACTACTGATCCCGCGGCTCCAGG 60
Db 37 AGCTGAGCTCCACCGGCTGGCGGCGCTCTAGAACTACTGATCCCGCGGCTCCAGG 60
QY 61 AATTCGGCAGG 73
Db 97 AATTCGGCAGG 109

RESULT 14

US-09-060-208-1
Sequence 1, Application US/09060208
Patent No. 6221629

GENERAL INFORMATION:

APPLICANT: Marshall, Lisa
APPLICANT: Roshak, Amy
TITLE OF INVENTION: THE DNA SEQUENCE OF HUMAN RP-105
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: USA
ZIP: 19482-0980

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,208
FILING DATE: April 15, 1998

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Prestia, Paul F.
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: P0380-1
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 2775 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:

US-09-060-208-1

Query Match 4.1%; Score 73; DB 4; Length 2775;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGCTCCACCGGCTGGCGGCGCTCTAGAACTACTGATCCCGCGGCTCCAGG 60
Db 37 AGCTGAGCTCCACCGGCTGGCGGCGCTCTAGAACTACTGATCCCGCGGCTCCAGG 60

QY 61 AATTCGGCAGG 73
Db 97 AATTCGGCAGG 109

RESULT 15

US-08-472-934-5
Sequence 5, Application US/08472934
Patent No. 575346

GENERAL INFORMATION:

APPLICANT: JOHNSON, GARY L.
TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING CELL
RESPONSIVENESS TO EXTERNAL SIGNALS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive and Cockfield
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,934
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/440,421
FILING DATE: 15-May-1995
PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: 08/354,516

FILING DATE:

FILING DATE: 21-FEB-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 5,405,941

FILING DATE:

FILING DATE: 15-APR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/323,460

FILING DATE:

FILING DATE: 14-Oct-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/11690

FILING DATE:

FILING DATE: 14-Oct-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/04178

FILING DATE:

FILING DATE: 15-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Giulio A. DeConti, Jr., Esq.

REGISTRATION NUMBER:

REGISTRATION NUMBER: 31,503

REFERENCE/DOCKET NUMBER:

REFERENCE/DOCKET NUMBER: CPI-004DVCP2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 3089 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 400..2280

US-08-472-934-5

Query Match 4.1%; Score 73; DB 1; Length 3089;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATTCGAGCTCCACCGGCTGGCGGCGCTCTAGAACTACTGATCCCGCGGCTCCAGG 60
Db 37 AATTCGAGCTCCACCGGCTGGCGGCGCTCTAGAACTACTGATCCCGCGGCTCCAGG 60

Db 11 AGCTGGAGCTCCACCGGGGTTGGGCGCTCTAGAACTAGTGGATCCCCCGGGCTGGCAGG 70
Qy 61 AATTGGGCACGAG 73
Db 71 AATTGGGCACGAG 83

Search completed: October 31, 2002, 10:33:20
Job time : 92 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 31, 2002, 09:41:15 : Search time 3203 seconds
(without alignments)
16098 619 Million cell updates/sec

Title: US-09-854-300-7
Perfect score: 1774
Sequence: 1 agatgaagctccacggggt : aggregated sequence 1774

Scoring table: OLTGO_NMR
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: listing first 75 summaries

Database :

GenEmbl:

1: gb_ba:
2: gb_hlg:
3: gb_in:
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12: gb_sy:
13: gb_un:
14: gb_vi:
15: em_ba:
16: em_fun:
17: em_hum:
18: em_in:
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26: em_ro:
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32: em_htg_other:
33: em_htg_mus:
34: em_htg_pln:
35: em_htg_rod:
36: em_htg_mam:
37: em_htg_vrt:
38: em_sy:
39: em_htgo_hum:
40: em_htgo_mus:
41: em_htgo_other:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1417	79.9	2796	6	AX337968 Sequence
2	1336	75.3	2830	9	AK074264 Homo sapi
3	715	40.3	1297	9	AF394689 Homo sapi
4	625	35.2	169812	9	AL391315 Human DNA
5	625	35.2	169863	2	AL591467 Homo sapi
6	395	22.3	1871	9	AK027169 Homo sapi
7	292	16.5	404	6	AX071980 Sequence
8	275	15.5	646	6	AX341568 Sequence
9	167	9.4	435	6	AX369681 Sequence
10	77	4.3	912	6	AX087649 Sequence
11	76	4.3	1585	8	OSCHINDPR
12	75	4.2	1605	6	AX027925 Sequence
13	74	4.2	851	3	FE786120
14	74	4.2	1190	6	AB4916 Sequence 7
15	74	4.2	1701	6	AX210670 Sequence
16	74	4.2	1701	9	AB028859 Homo sapi
17	74	4.2	1798	8	ATCFC2B
18	74	4.2	2448	4	OCU132110
19	74	4.2	2605	6	AR070327 Sequence
20	73	4.1	518	8	AB005878 Nicotiana
21	73	4.1	545	6	AR184181 Sequence
22	73	4.1	742	6	AX406874 Sequence
23	73	4.1	1365	3	PD0316541
24	73	4.1	1388	6	AX101122 Sequence
25	73	4.1	1556	6	A62300 Sequence 3
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27	73	4.1	1568	6	A62298 Sequence 1
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29	73	4.1	1585	6	AP202707 Sequence
30	73	4.1	1585	6	AX134055 Sequence
31	73	4.1	1585	6	AX286133 Sequence
32	73	4.1	1724	8	AB075903 Avicennia
33	73	4.1	1731	10	AY012159 Mus muscu
34	73	4.1	2046	8	AF060519 Cuphea ho
35	73	4.1	2186	3	PVA250829
36	73	4.1	2503	6	AX033851 Sequence
37	73	4.1	2775	6	AX018138 Sequence
38	73	4.1	3089	6	AR008278 Sequence
39	73	4.1	3089	6	AR068732 Sequence
40	73	4.1	3089	6	AR085074 Sequence
41	73	4.1	3089	6	AR098267 Sequence
42	73	4.1	3089	6	AR181005 Sequence
43	73	4.1	3328	6	AR164434 Sequence
44	73	4.1	3514	6	AX451794 Sequence
45	73	4.1	4483	9	AF058696 Homo sapi
46	73	4.1	120793	2	AF322450 Homo sapi
47	72	4.1	1711	6	A82595 Sequence 3
48	72	4.1	1711	6	A82786 Sequence 1
49	71	4.0	1179	8	AF315589 Fetunia x
50	71	4.0	2045	6	AF156902 Sequence
51	70	3.9	562	3	DMELAST
52	70	3.9	1352	8	THA243514 Trichoder
53	70	3.9	1387	6	AX047063 Sequence
54	70	3.9	1424	6	AX180959 Sequence
55	70	3.9	1460	6	AX047064 Sequence
56	70	3.9	1815	8	AB075902 Avicennia
57	70	3.9	1972	8	THA269534 Trichoder
58	70	3.9	2085	6	AR060385 Sequence
59	68	3.8	1169	6	AX364844 Sequence
60	68	3.8	2021	5	AB070851 Xenopus l
61	68	3.8	2993	6	AX021518 Sequence
62	68	3.8	3050	4	AF033623 Ovis arie
63	67	3.8	500	6	AR169202 Sequence
64	67	3.8	500	6	AR182492 Sequence
65	67	3.8	500	6	AR194875 Sequence


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DB 1528 ACCATTATTAATAAATAGAACTGTAATCAGAGGATTAATTTATTATAAATAATGSAATAA 1547
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DB 1634 TTTATAAAATAACAGTATACATAAAAGTCTCATATCACTAATAATATAGTATAGTAA 1643
QY
DB 1588 TTTATAAAATAAGAGTATACATAAAAGTCTCATATCACTAATAATATAGTATAGTAA 1647
QY
QY 1644 A 1644
DB 1648 A 1648

RESULT 2
AK074264 2830 bp mRNA linear FEB 15-FEB-2002
LOCUS Homo sapiens cDNA FL127464 fis. clone HEP09821
DEFINITION AK074264
ACCESSION AK074264
VERSION AK074264.1 GI:14676819
KEYWORDS oligo capping; fis (full insert sequence);
SOURCE Homo sapiens RefSeq: chr11:114,444,444-114,444,444; HEP09821; HEP
clone:HEP09821.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Cnidaria; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1
REFERENCE
AUTHORS Kawabata A., Hiraji T., Kobayashi M., Inagaki M., Ikawa Y.,
Okamoto S., Ohtsuka T., Ota T., Suzuki Y., Ohashi M., Nishi T.,
Shibahara T., Tanaka T., Nakamura Y., Isoda T. and Sugano S.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2830)
AUTHORS Sugano S., Suzuki Y., Ota T., Kobayashi M., Nishi T., Isoda T.,
Shibahara T., Tanaka T. and Nakamura Y.
DIRECT SUBMISSION
SUBMITTED (14-FEB-2002) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure, Human Gene-
Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
(E-mail: cdna@ims.u-tokyo.ac.jp, Tel: 81-3-5449-5296,
Fax: 81-3-5449-5416)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing;
Research Association for Biotechnology: cDNA library construction,
5'- & 3'-end one pass sequencing; Department of Virology and Human
Genome Center, Institute of Medical Science, University of Tokyo
(partly supported by Science and Technology Agency).
FEATURES
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CAVCLIELKNDLVLPILTONHIFHKTCVDPWLLHPTCPMKCDILKALGIEVDVGG
SVSLQVPSNFISNSASHEFDNPSFASYSASVQQLRPFILFHVLSPIRSLQVIR
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BASE COUNT 927 a 564 c 530 g 804 *
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Query Match 75.3% Score 1326; DB 9; Length 2830;
Best Local Similarity 94.7%; Pred No 0;
Matches 1586; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 181 AAATCTGTGTAATAAGAAAAGTTGACCAATTAGTAATAACAGAACTGCCAATCAGGSCCT 240
QY 1609 AGTTTCTATTATAAATGGTAATAATTTAATAAATAGAGTGTATAGTAAAGTGCTCAG 1668
Db 241 AGTTTCTATTATAAATGGTAATAATTTAATAAATAGAGTGTATAGTAAAGTGCTCAG 300
QY 1669 ATGACTAATATATGCTATAGTAA 1694
Db 301 ATGACTAATATATGCTATAGTAA 326

RESULT 9
LOCUS AX396961 435 bp DNA linear PAT 18-MAY-2002
DEFINITION Sequence 1176 from Patent WO0212328.
ACCESSION AX396961
VERSION AX396961.1 GI:21067708
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1.
AUTHORS King G.E., Weagher M.J., Xu J. and Secriest H.
TITLE Compositions and methods for the therapy and diagnosis of colon cancer
JOURNAL Patent: WO 0212328-A 1176 14-FEB-2002.
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source Location/Qualifiers
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BASE COUNT 147 a 62 c 69 g 157 t
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Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 TTTTCGAGAAATTAATCTTAAATCTGTGTATATAGAAACCTGACCAATTAATTAATAA 1587
Db 337 TTTTCGAGAAATTAATCTTAAATCTGTGTATATAGAAACCTGACCAATTAATTAATAA 228
QY 1588 CAGAACTGTGATAGAGCTAGCTTTTATTATAAATTCATATAATTTAATAATAAATAC 1647
Db 277 CAGAACTGTGATAGAGCTAGCTTTTATTATAAATTCATATAATTTAATAATAAATAC 218
QY 1648 AGTGATCTGAAGTGTGATGATGATCAATATATATGCTATAGTAA 1694
Db 217 AGTGATCTGAAGTGTGATGATGATCAATATATATGCTATAGTAA 171

RESULT 10
LOCUS AR087649 912 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 3 from patent US 5989549.
ACCESSION AR087649
VERSION AR087649.1 GI:10014412
KEYWORDS unknown.
SOURCE unknown.
ORGANISM unknown.
REFERENCE 1 (bases 1 to 912)
AUTHORS Sullivan P., Berube R., Legare C. and Gaudreault C.
TITLE Acrosomal sperm protein and uses thereof
JOURNAL Patent: US 5989549-A 3 24-NOV-1999.
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BASE COUNT 187 a 279 c 286 g 160 t
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Best Local Similarity 100.0%; Pred. No. 5.5e-33;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGACTCCAGCGGCTGCGCGGCTCTAGAACTAGTATCCCGCGGCTGCAGG 60
Db 7 AGCTGAGACTCCAGCGGCTGCGCGGCTCTAGAACTAGTATCCCGCGGCTGCAGG 66
QY 61 AATTCGGCAGCAGCCGA 77
Db 67 AATTCGGCAGCAGCCGA 83

RESULT 11
LOCUS OSCHINDP 1585 bp mpna linear PLN 11-SEP-1995
DEFINITION O.sativa mRNA for chilling-inducible protein.
ACCESSION Z54153
VERSION Z54153.1 GI:984755
KEYWORDS
SOURCE Oryza sativa (Japonica cultivar-group).
ORGANISM Oryza sativa (Japonica cultivar-group)
REFERENCE 1.
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzoae; Oryza.
TITLE Complete sequence of a cDNA related to chilling tolerance in rice
JOURNAL Binh L.
REFERENCE 1 (bases 1 to 1585)
AUTHORS
TITLE Complete sequence of a cDNA related to chilling tolerance in rice
JOURNAL Binh L.
REFERENCE 2 (bases 1 to 1585)
AUTHORS Binh L. and Oono K.
TITLE Molecular cloning and characterization of genes related to chilling tolerance in rice
JOURNAL Plant Physiol. 99, 1146-1150 (1992)
REMARK (sites)
REFERENCE 3 (bases 1 to 1585)
AUTHORS Binh L.
TITLE Direct Submission
JOURNAL Submitted (11-SEP-1995) Binh L., Institute of Biotechnology (IBT),
MST, Plant Cell Biotechnology, Nghiado, Tuliem, Hanoi, Vietnam,
10000
FEATURES
source Location/Qualifiers
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GSAPKPLQKSSPIKEPKPPPHSSGLSAPIELGDLRLMKEKREGMYVYLIGS
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QY 61 AATTGGGACGAGCG 76
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Db 9R AATTGGGACGAGCG 113

RESULT 12
AX027925
LOCUS EV 1 1605 bp DNA linear PAT 16 SEP 2000
DEFINITION Sequence 1 from Patent EP1002465
ACCESSION AX027925
VERSION AX027925.1 GI:10188750
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1605)
AUTHORS Fraser,R., Guillot,E. and Angel,I.
TITLE Adipose specific protein
JOURNAL Patent: EP 1002465-A 1 24-MAY-2000;
SANOFI SYNTHELABO (FR)
FEATURES
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Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 60
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Db 227 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 246
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QY 61 AATTGGGACGAGCG 75
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Db 297 AATTGGGACGAGCG 301

RESULT 13
TE286120
LOCUS TE286120 851 bp mRNA linear INV 13-MAR-1997
DEFINITION TE286120 TE286120
ACCESSION TE286120
VERSION TE286120.1 GI:1460243
KEYWORDS Trypanosoma evansi.
SOURCE Trypanosoma evansi.
ORGANISM Trypanosoma evansi.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE 1 (bases 1 to 851)
AUTHORS Boid,R., Munro,A., Luckins,A.G. and Jones,T.W.
TITLE Sequence characterisation of putative antigens of Trypanosoma
evansi (Indonesia)

Best Local Similarity 100.0%; Pred No. 2 3e-32;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 AATTGGGACGAGCG 76
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Db 9R AATTGGGACGAGCG 113

RESULT 14
AX04916
LOCUS AX04916 1190 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 7 from Patent WO9844104.
ACCESSION AX04916
VERSION AX04916.1 GI:6733757
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1190)
AUTHORS Schroeder,M. and Streiner,V
TITLE FLIP GENE AND FLIP PROTEIN
JOURNAL Patent: WO 984104-A 7 08-OCT-1998;
SCHROEDER MICHAEL (CH); STFINER VERONIQUE (CH)
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BASE COUNT 361 a 249 c 280 g 300 t
ORIGIN

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Best Local Similarity 100.0%; Pred No. 3.4e-31;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 45 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 94
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QY 61 AATTGGGACGAGCG 74
|||||
Db 9R AATTGGGACGAGCG 108

RESULT 15
AX210670
LOCUS AX210670 1701 bp DNA linear PAT 31-AUG-2001
DEFINITION Sequence 312 from Patent WO0157058.
ACCESSION AX210670
VERSION AX210670.1 GI:15424930
KEYWORDS

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SOURCE
ORGANISM      human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae, Homo.
REFERENCE
1 (bases 1 to 1701)
AUTHORS      Rosenthal A., Hinzmann B., Schaefer R., Zuber J., Tchernitsa O.,
Grips M., Hellriegel M., Schmitz A.C. and Sers C.
TITLE        Detection of differential gene expression
JOURNAL      Patent: WO 0157058-A 312 09-AUG-2001;
Metagen Gesellschaft fuer Genomforschung mbH (DF)
FEATURES
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Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 9 AGCTGAGTCTTAAAGCTGAGTGGCTGAGTCTTAAAGACTAGTGGATGCTCCCGGCGTGCAGG 68
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QY 61 AATTGGGACGAGC 74
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DB 69 AATTGGGACGAGC 82
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RESULT 17
LOCUS      ABC28859              1701 bp  mRNA  linear  FRI 14-DEC-1999
DEFINITION Homo sapiens mRNA for hDj9, complete cds.
ACCESSION  AB028859
VERSION    AB028859.1 GI:6567165
KEYWORDS   hDj9.
SOURCE     Homo sapiens cDNA to mRNA, clone_lib:Stratagene pancreas.
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE  1 (sites)
AUTHORS    Ohtsuka K. and Hata M.
TITLE      Mammalian HSP40/DNAJ homologs: Cloning of novel cDNAs and proposal
for the classification and nomenclature
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 1701)
AUTHORS    Ohtsuka K
TITLE      Direct Submission
JOURNAL    Submitted (10-JUN-1999) Kenzo Ohtsuka, Aichi Cancer Center Research
Institute, Laboratory of Experimental Radiobiology, 1-1 Funakubo,
Chikusa-ku, Nagoya, Aichi 464-8681, Japan
(E-mail: khtsuka@ichi-cc.pref.aichi.jp)
Tel:81 2-763-6111(ex.8845), Fax:81 52-763-5233
FEATURES
Location/Qualifiers
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TRANSLATION

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GDIPSHFGDFGFMFGGTGPGQDNIIPGSDIIVDLVLTLEEVYAGNFVYVNRKPVV
PQAGKGCNCPCMRGTQTGPGFQMTQVQVDECPNVKLVNEERTLEVELEGVVD
GMGEYFEGEGPHVDGEGDLRFKIKVWHFIFERBCDLYTNVTLSLVESLVGPEMD
ITHLDGHVHISRDKIIRPGAKLWKKGEGLPNFDNNIKSLIITFDVFPPEQLEET
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306..515
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/note="J domain"
BASE COUNT   489 a 321 c 471 g 420 t
ORIGIN
Query Match      4.2%; Score 74; DP 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 3.5e-31;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCTGAGTCTTAAAGCTGAGTGGCTGAGTCTTAAAGACTAGTGGATGCTCCCGGCGTGCAGG 60
|||||
DB 9 AGCTGAGTCTTAAAGCTGAGTGGCTGAGTCTTAAAGACTAGTGGATGCTCCCGGCGTGCAGG 68
|||||
QY 61 AATTGGGACGAGC 74
|||||
DB 69 AATTGGGACGAGC 82
|||||
RESULT 17
LOCUS      ATCYC2R              1798 bp  mpna  linear  FLN 24-NOV-1994
DEFINITION A.thaliana (Columbia) cyc2b mpna for cyclin 2b protein.
ACCESSION  Z31401
VERSION    Z31401.1 GI:509422
KEYWORDS   cyc2b gene; cyclin 2b.
SOURCE     thale cress.
ORGANISM   Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE  1 (bases 1 to 1798)
AUTHORS    Van Montagu M.
TITLE      Direct Submission
JOURNAL    Submitted (22-MAR-1994) Van Montagu M., Rijksuniversiteit Gent,
Laboratory of Genetics, Ledeganckstraat, 35, Gent, Belgium, B-9000
2 (bases 1 to 1798)
AUTHORS    Ferreira P., Hemery A., de Almeida Engler J., Bergounioux C.,
Bursens S., Van Montagu M., Engler G. and Inze D.
TITLE      Three discrete classes of Arabidopsis cyclins are expressed during
different intervals of the cell cycle
JOURNAL    Proc. Natl. Acad. Sci. U.S.A. 91 (24), 11313-11317 (1994)
MEDLINE    95062258
PUBMED     7972055
FEATURES
Location/Qualifiers
1..1798
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="cyc2bat"
/tissue_type="cell suspensions"
/clone_lib="cell suspension Lambda ZapII"
248..1537
/gene="cyc2b"
248..1537
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/function="regulatory subunit of cyclin dependent
complexes"
/codon_start=1
/product="cyclin 2b protein"
/protein_id="CAA83276.1"
/db_xref="GI:509423"
/translation="MNVFENNVLVVKPIITLIDDPKPSKFGVEMKRNPPALGV
TNHNVIAKAPKVVNKKPGLSPKPSLSTKFKLSLHPSISPSQETKRLKPSGNEF
GSLIFDEEEKNEEVILQFMPMSLERYIEFLPMEEEVEEMLEERPEEVLDIDG

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Db 1 GCTGGAGTCCACCGCGTGGCGCGCTGTAGAACTAGTATGATGCGCGCGTGGCGCGG 60
QY 62 ATTCGGCAGCAGC 74
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Db 61 ATTCGGCAGCAGC 73
      |||||

RESULT 24
LOCUS AX101122 1388 bp DNA linear PAT 10-APR-2001
DEFINITION Sequence 1 from Patent WO0121650.
ACCESSION AX101122
VERSION AX101122.1 GI:13619973
KEYWORDS
SOURCE
ORGANISM
  Dimorphotheca.
  Dimorphotheca
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta, eudicotyledons, core eudicots;
  Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;
  Calenduleae.
  1 (bases 1 to 1388)
  Coldren,C., Flint,D., Hallahan,D.L. and Wang,H.
  Cis-prenyltransferases from plants
  Patent: WO 0121650-A 1 29-MAR-2001;
  E.I. DU PONT DE NEMOURS AND COMPANY (US)
FEATURES
  source
    1..1388
    /db_xref="taxon:13490"
    /organism="Dimorphotheca"
BASE COUNT 437 a 268 c 297 g 386 t
ORIGIN
Query Match 4 1%; Score 73; DB 6; Length 1388;
Best Local Similarity 100.0%; Pred. No. 1.3e-30;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCTGGAGTCCACCGCGTGGCGCGCTGTAGAACTAGTATGATGCGCGCGTGGCGCGG 61
Db 213 GCTGGAGTCCACCGCGTGGCGCGCTGTAGAACTAGTATGATGCGCGCGTGGCGCGG 272
QY 62 ATTCGGCAGCAGC 74
      |||||
Db 273 ATTCGGCAGCAGC 285

RESULT 25
LOCUS A62300 1556 bp DNA linear PAT 09-MAR-1998
DEFINITION Sequence 3 from Patent WO9712982.
ACCESSION A62300
VERSION A62300.1 GI:3716263
KEYWORDS
SOURCE
ORGANISM
  unidentified.
  unidentified
  unclassified.
  1 (bases 1 to 1556)
  Boudet,A., Pichon,M., Grima-Pettenati, Jacqueline, Beckert,M.,
  Gamas,P., Briat and Jean-Francois.
  DNA SEQUENCES CODING FOR A CINNAMOYL COA REDUCTASE, AND
  APPLICATIONS THEREOF IN THE CONTROL OF LIGNIN CONTENTS IN PLANTS
  Patent: WO 9712982-A 3 10-APR-1997;
  CENTRE NAT RECH SCIENT (FR)
  other publication FR 2739395 970404.
FEATURES
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    1..1556
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    /db_xref="gi:3716263"
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    /protein_id="CAA03626.1"
    /db_xref="gi:3716263"
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VFLLKLVGYTVKGVTRNPQCPKNAHLKALINGAAEPLTICWADLIDYCAICPAVQCGCG
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VWUESWSELEHTEKTKNNKYCYKAVAEJAAEAAKKGVLVNVNVLVVGKLLQAT
VNASIAHLKLDGSAFTFANAVQATVDVADAHLRVFPSPRSGRLCAERVLHR
EDVVRILAKLFPEYPPARCSEVNPKPQYKFSNGLKMLDGLQFPFVPSUSLYUTVKN
LOEKRLHPVLGERTITTAADKAPAAEMOOGGIAIRA"
BASE COUNT 304 a 500 c 505 g 247 t
ORIGIN
Query Match 4.1%; Score 73; DB 6; Length 1556;
Best Local Similarity 100.0%; Pred. No. 1.3e-30;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGTCCACCGCGTGGCGCGCTGTAGAACTAGTATGATGCGCGCGTGGCGCGG 60
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Db 52 AGCTGGAGTCCACCGCGTGGCGCGCTGTAGAACTAGTATGATGCGCGCGTGGCGCGG 111
QY 61 AATTCGGCAGCAGC 73
      |||||
Db 112 AATTCGGCAGCAGC 124

RESULT 26
LOCUS ARI45428 1556 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 3 from patent US 6211432.
ACCESSION ARI45428
VERSION ARI45428.1 GI:15107295
KEYWORDS
SOURCE
ORGANISM
  Unknown.
  Unclassified.
  1 (bases 1 to 1556)
  Boudet,A., M., Pichon,M., Grima-Pettenati,J., Beckert,M., Gamas,P.
  and Briat,J.-F.
  DNA sequences coding for a cinnamoyl CoA reductase, and
  applications thereof in the control of lignin contents in plants
  Patent: US 6211432-A 3 03-APR-2001;
  Location/Qualifiers
    1..1556
    /organism="unknown"
BASE COUNT 304 a 500 c 505 g 247 t
ORIGIN
Query Match 4.1%; Score 73; DB 6; Length 1556;
Best Local Similarity 100.0%; Pred. No. 1.3e-30;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGTCCACCGCGTGGCGCGCTGTAGAACTAGTATGATGCGCGCGTGGCGCGG 60
      |||||
Db 52 AGCTGGAGTCCACCGCGTGGCGCGCTGTAGAACTAGTATGATGCGCGCGTGGCGCGG 111
QY 61 AATTCGGCAGCAGC 73
      |||||
Db 112 AATTCGGCAGCAGC 124

RESULT 27
LOCUS A62298 1569 bp DNA linear PAT 06-MAR-1998
DEFINITION Sequence 1 from Patent WO9712982.
ACCESSION A62298
VERSION A62298.1 GI:3716261
KEYWORDS
SOURCE
ORGANISM
  unidentified.
  unidentified
  unclassified.
  1 (bases 1 to 1568)
  Boudet,A., Pichon,M., Grima-Pettenati, Jacqueline, Beckert,M.,
  Gamas,P., Briat and Jean-Francois.
  DNA SEQUENCES CODING FOR A CINNAMOYL COA REDUCTASE, AND
  APPLICATIONS THEREOF IN THE CONTROL OF LIGNIN CONTENTS IN PLANTS
  Patent: WO 9712982-A 1 10-APR-1997;

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COMMENT CENTRE NAT RECH SCIENT (FR)
Other publication PP 2739395 970404
FEATURES Location/Qualifiers
1..1568
/organism="unidentified"
/db_xref="taxon:32644"

CDS
278..11306
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CYFTNNYCYGYAVAAEAADVAKEGVDLVVYFVVLVGLQFTIRASTHILKYL
TGSAPTKANATQAVVHVDRVALAHILVYKPSAGRYLCAETSLHGRVLVEILAYFP
EYPIPTCKSEKNDPPVPHIFSFKFLKDLQLEFTVPVSECLYEVKSLQCHLSIFNK
EDSLAVKS"

BASE COUNT 478 a 335 c 336 g 419 t

Query Match 4.1%; Score 73; DB 6; Length 1568;

Best Local Similarity 100.0%; Pred. No. 1.4e-30;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACGGCGGTGGCGGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 60
Db 47 AGCTGGAGCTCCACGGCGGTGGCGGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 106

QY 61 AATTCGGCAGGAG 73

Db 107 AATTCGGCAGGAG 119

RESULT 28

LOCUS AX134055

DEFINITION Sequence 1 from patent US 6211432.

ACCESSION AX134055

VERSION AX134055.1 GI:15107294

KEYWORDS

SOURCE

ORGANISM

Unidentified.

REFERENCE 1 (bases 1 to 1568)

AUTHORS Boudet, A.-M., Pichon, M., Grima-Pettenati, J., Beckert, M., Gamas, P.

and Briat, J.-F.

TITLE DNA sequences coding for a cinnamoyl CoA reductase, and

applications thereof in the control of lignin contents in plants

JOURNAL Patent: US 6211432-A 1 03-Apr-2001

FEATURES Location/Qualifiers

1..1568

/organism="unknown"

BASE COUNT 479 a 334 c 336 g 419 t

ORIGIN

Query Match 4.1%; Score 73; DB 6; Length 1568;

Best Local Similarity 100.0%; Pred. No. 1.4e-30;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACGGCGGTGGCGGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 60
Db 47 AGCTGGAGCTCCACGGCGGTGGCGGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 106

QY 61 AATTCGGCAGGAG 73

Db 107 AATTCGGCAGGAG 119

RESULT 29

LOCUS AR202707

DEFINITION Sequence 54 from patent US 6365165.

1585 bp DNA linear PAT 20-JUN-2002

ACCESSION AR202707

VERSION AR202707.1 GI:11448886

KEYWORDS

SOURCE

ORGANISM

Unknown.

Unidentified.

REFERENCE 1 (bases 1 to 1585)

AUTHORS Reed, S.G., Campos-Neto, A., Webb, J.P., Dillon, D.C. and Skeiky, Y.A.W.

TITLE Leishmania antigens for use in the therapy and diagnosis of

Leishmaniasis

JOURNAL Patent: US 6365165-A 54 02-Apr-2002;

FEATURES Location/Qualifiers

1..1585

/organism="unknown"

BASE COUNT 315 a 567 c 397 g 305 t

ORIGIN

Query Match 4.1%; Score 73; DB 6; Length 1585;

Best Local Similarity 100.0%; Pred. No. 1.4e-30;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3 AGCTGGAGCTCCACGGCGGTGGCGGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 62

QY 61 AATTCGGCAGGAG 73

Db 63 AATTCGGCAGGAG 75

RESULT 30

LOCUS AX134055

DEFINITION Sequence 54 from Patent EP1113073.

ACCESSION AX134055

VERSION AX134055.1 GI:14270210

KEYWORDS

SOURCE

ORGANISM

unidentified.

Unidentified.

FEATURES Location/Qualifiers

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/organism="unidentified"

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BASE COUNT 315 a 567 c 397 g 305 t

ORIGIN

Query Match 4.1%; Score 73; DB 6; Length 1585;

Best Local Similarity 100.0%; Pred. No. 1.4e-30;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACGGCGGTGGCGGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 60
Db 3 AGCTGGAGCTCCACGGCGGTGGCGGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 62

QY 61 AATTCGGCAGGAG 73

Db 63 AATTCGGCAGGAG 75

RESULT 31

LOCUS AX286133

DEFINITION Sequence 54 from Patent WO0179276.

ACCESSION AX286133

VERSION AX286133.1 GI:17046028

KEYWORDS

SOURCE

ORGANISM

Leishmania major.

Leishmania major

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Leishmania.

REFERENCE 1

AUTHORS Reed, S.G., Campos-Neto, A., Webb, J.P., Dillon, D.C., Skeiky, Y.A.,

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BASE COUNT      438 a    376 c    430 g    480 t
ORIGIN
Query Match.          4.1%, Score 73, DB 8, Length 1724;
Best Local Similarity 100.0%; pred. No. 1.4e-30;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


1 AGCTGGACGTCCTACCGAGTGTGGAGCGCGCTGTAGAATTAATGCATCCCTCCTGCTCAAG 60
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19 AGCTGGACGTCCTACCGAGTGTGGAGCGCGCTGTAGAATTAATGCATCCCTCCTGCTCAAG 78


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QY      61 AATTCGGACGAG 75
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Db      79 AATTCGSCACGAG 91

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RESULT 33
AY012159
LOCUS   1741 bp mDNA linear R2D 28-DEC-2000
DEFINITION Mus musculus virion-associated nuclear-shuttling protein mPNA,
partial cds.
ACCESSION AY012159
VERSION  AY012159.1 GI:11993888

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SOURCE	Mus musculus
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae, Mus. 1 (bases 1 to 1731)
AUTHORS	Gupta, K., Ott, D., Hope, T. J., Silliciano, R. and Boeke, J. D.
TITLE	A human nuclear shuttling protein that interacts with human immunodeficiency virus type 1 matrix is packaged into virions
JOURNAL	J. Virol. 74 (24), 11811-11824 (2000)
MEDLINE	20541981
PUBMED	11090181

Authors: Gupta, K.
 Title: Direct Submission
 Journal: Submitted (06-SEP-2000) Department of Molecular Biology and Genetics, Johns Hopkins University School of Medicine, 725 N. Wolfe St., Hutterian 6.4, Baltimore, MD 21205, USA
 Features: Location/Qualifiers
 1..1731
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 <1..1731
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 /codon_start=1
 /product="viral-associated nuclear-shuttling protein"
 /protein_id="AAC42155.1"
 /db_xref="GI:11993889"

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TNSNMEKPEPASKSPGSCNAGSSDFEVVPTTEQSONSPETGSHPTNMMDLGGPPPPEDSNLKI
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ENEALEKALMGKGLGEGDGLAENRPEPTTEKLLLNNSCKEGLCQAPSSPKPFGGAKK
GATGQQQASVMASKVTEAGAFGAAGFVKVLLCQPPRFLFVNFQCHPSPKSHKQQQTEK
KITELRQKLVDQKQVTEAEFEQQRDFDRKLLKLLKLEEMBEEDKQSLTAKEEL
RUKVRYLQQLSLQVREYQKEIKUNKALEEALSUAQSSPPAQSPEGVGGH
LPKQELVTQELLKQVQKIFEEQDFSDREPMNDEEELKKQVBEKLAQVTLTNAQ
LKTLEEKSKAKALKQQRKASGKERYHMEPHPEHVCGAYPYAPPPMPAMPYHAYK
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EPADLRLPKV*
470 a 509 c 503 g 249 t

Query Match 4 1%; Score 73; DB 10; Length 1731;
1 Best Local Similarity 100.0%; Pred. No. 1.4e-30;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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cu 11 AGCTGAACTCCATCCGCGGTGGGCGGCTGCTATASAACTAGTGTGATCCCGCGGCTCGAGG 70
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QY 61 AATTCGGCAGGAG 73
|||||
Db 71 AATTCGGCAGGAG 83

RESULT 34
AF060519
DEFINITION
  Cuphea hookeriana 3-ketoacyl-ACP synthase (Kas4) cDNA, complete
  cds.
  2046 bp mRNA linear PLN 28 OCT-1998
ACCESSION
  AF060519
VERSION
  AF060519.1 GI:3800748
KEYWORDS
  Cuphea hookeriana.
SOURCE
  Cuphea hookeriana.
  Eukaryota: Viridiplantae; Streptophyta: Embryophyta: Tracheophyta:
  Spermatophyta: Magnoliophyta: eudicotyledons: Core eudicots:
  Rosidae: eurosids II: Myrtales: Lythraceae: Cuphea.
REFERENCE
  1 (bases 1 to 2046)
  Rehesh, K., Edwards, P., Fillatti, J., Slabaugh, M. and Byrne, J.
  KAS IV: a 3-ketoacyl-ACP synthase from Cuphea sp. is a medium chain
  specific condensing enzyme
  Plant J. 15 (3). 383-390 (1998)
JOURNAL
  MEDLINE
  98422743
PUBMED
  9750349
REFERENCE
  2 (bases 1 to 2046)
  Dehesh, K.
  Direct Submission
  Submitted (20-APR-1998) Gills division, Calgene, 1420 Fifth Street,
  Davis, CA 9561, USA
  Location/Qualifiers
  1..2046
  /organism="Cuphea hookeriana"
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  125..1729
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  DCSQPTPIAGEIKFSTGDAVPKFEPMDFMLYMLTAGKALADGSGTDEAMKEL
  NKRKGVLIGSLGGMVFVSUSIEALRTSYKKISPFQVPSSTTNMGSAILAMDLMGM
  PNYSTACATSNFCILNAANHIIKGEADMCLGGSDAALVPLVGLGFVACRALSORN
  NDPTKASRPWQSNRDPGFVYMGCAVLIIIELEHAKKPCATLIYAEFLGSGSTCCAYHWT
  EHPFGAGVILICAKLAQSVSRFDVNYINAHATSTPAGDINKEYQALAHCPQNSSEL
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  ORIGIN
  418: Score 73; DB 8; Length 2046;
  Query Match
  Best Local Similarity 100.0%; Pred. No. 1.4e-30;
  Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGTTCACCGGCTGAGCGGCTCTTAGAACTAGTGGATGCGCGGCGGAGG 73
|||||
Db 16 AGCTGGAGTTCACCGGCTGAGCGGCTCTTAGAACTAGTGGATGCGCGGCGGAGG 83

QY 61 AATTCGGCAGGAG 73
|||||
Db 76 AATTCGGCAGGAG 88

RESULT 35
PVA250829
LOCUS
  PVA250829
  2186 bp mRNA linear INV 04-APR-2000
  418: Score 73; DB 3; Length 2186;
  Query Match
  Best Local Similarity 100.0%; Pred. No. 1.4e-30;
  Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGTTCACCGGCTGAGCGGCTCTTAGAACTAGTGGATGCGCGGCGGAGG 60
|||||
Db 27 AGCTGGAGTTCACCGGCTGAGCGGCTCTTAGAACTAGTGGATGCGCGGCGGAGG 86

QY 61 AATTCGGCAGGAG 73
|||||
Db 87 AATTCGGCAGGAG 99

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DEFINITION
  Penaeus vannamei mRNA for phosphoenolpyruvate carboxykinase (pepck
  gene).
ACCESSION
  AJ250829
VERSION
  AJ250829.1 GI:7414465
KEYWORDS
  pepck gene; phosphoenolpyruvate carboxykinase.
SOURCE
  Litopenaeus vannamei.
ORGANISM
  Litopenaeus vannamei.
  Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
  Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
  Penaeidae; Litopenaeus.
  1 (bases 1 to 2186)
  Van Wormhoudt, A.E. and Arena Ortiz, M.L.
  Characterization of phosphoenolpyruvate carboxykinase from Penaeus
  vannamei (Crustacea Decapoda)
  Unpublished
  2 (bases 1 to 2186)
  Van Wormhoudt, A.E.
  Direct Submission
  Submitted (02-NOV-1999) Van Wormhoudt A.E., Museum National
  d'Histoire Naturelle, CNRS, BP 270, 29900 Concarneau, FRANCE
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  /country="French Polynesia:Panama"
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  /evidence="experimental"
  /product="phosphoenolpyruvate carboxykinase"
  /protein_id="CAB85964.1"
  /db_xref="GI:7414466"
  /translation="MLLFLRLNGVLGEARVAEANKLNLAFAQSLATIHGSLSLDK
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  YVVPFSGVPGSPILSKIQLTDSYVYVASMRTMRMGKAVLDALAEODFVKCLHVG
  CPLPLQRTLNNMPCDPERTIVTHVPTSETISPGSGYGGNTLLGKKKSLPGSTIAL
  REDWLAELHLLIGITNGQEVAKYIAALPSACGSTNLAMMTPLALPKYKVCVDDIAN
  IKFDDGVLRALINPENGFGVAPGTSMTHTNPVAMQTVLSNTIFTNVAKTSDGGVFWEG
  LEKETANDVTTISWLDGNTNSKSGKPAAPHNSLFCPTAGOSPTIDPAWEDPKGVHIS
  AILGRRRPEGVPLIYFAFSWKGVLVGGAMRSPTAAAEHAKVIMHDFAMRPFPG
  YNFHYLQHLWSMTRTHKALPKIFHVNWPKDEKARFIWPGFGENDRVLDWILRRVD
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  /evidence="experimental"
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  /gene="pepck"
  /product="phosphoenolpyruvate carboxykinase"
  /EC_number="4.1.1.32"
  /evidence="experimental"
  510 a 668 c 605 g 403 t
BASE COUNT
  ORIGIN
  418: Score 73; DB 3; Length 2186;
  Query Match
  Best Local Similarity 100.0%; Pred. No. 1.4e-30;
  Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGTTCACCGGCTGAGCGGCTCTTAGAACTAGTGGATGCGCGGCGGAGG 60
|||||
Db 27 AGCTGGAGTTCACCGGCTGAGCGGCTCTTAGAACTAGTGGATGCGCGGCGGAGG 86

QY 61 AATTCGGCAGGAG 73
|||||
Db 87 AATTCGGCAGGAG 99

```

```

RESULT 36
AX033851
LOCUS AX033851 2500 bp DNA linear PAT 21-SEP-2000
DEFINITION Sequence 1 from Patent NO944851.
ACCESSION AX033851
VERSION AX033851.1 GI:10280444
KEYWORDS
SOURCE Neocallimastix patriciarum.
ORGANISM Neocallimastix patriciarum.
REFERENCE Neocallimastix patriciarum.
AUTHORS Eukaryota; Fungi; Chytridiomycota; Neocallimastix.
JOURNAL Neocallimastixaceae; Neocallimastix.
FEATURES
BASE COUNT 893 a 389 c 517 g 704 t
ORIGIN
Query Match 4.1%; Score 73; DB 6; Length 2503;
Best Local Similarity 100.0%; Pred. No. 1.4e-30;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCTGAGCTCCACCGGGTGGGGGCTCTAGAACTAGTGGATCCCGGGGTTGCGAGG 60
DB 52 AGCTGAGCTCCACCGGGTGGGGGCTCTAGAACTAGTGGATCCCGGGGTTGCGAGG 111
QY 61 AATTCGGCAGCAG 73
DB 112 AATTCGGCAGCAG 124

RESULT 37
AX018138
LOCUS AX018138 2775 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 1 from patent US 5780609
ACCESSION AX018138
VERSION AX018138 1 GI:3074741
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2775)
AUTHORS Marshall, L.A. and Poshak, A.K.
TITLE DNA sequence of human RP-105
JOURNAL Patent: US 5780609-A 1 14-JUL-1998;
FEATURES
BASE COUNT 702 a 534 c 565 g 724 t
ORIGIN
Query Match 4.1%; Score 73; DB 6; Length 2775;
Best Local Similarity 100.0%; Pred. No. 1.4e-30;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCTGAGCTCCACCGGGTGGGGGCTCTAGAACTAGTGGATCCCGGGGTTGCGAGG 60
DB 37 AGCTGAGCTCCACCGGGTGGGGGCTCTAGAACTAGTGGATCCCGGGGTTGCGAGG 96
QY 61 AATTCGGCAGCAG 73
DB 97 AATTCGGCAGCAG 109

RESULT 38
AP008278
LOCUS AP008278 3089 bp DNA linear PAT 04-SEP-1999
DEFINITION Sequence 5 from patent US 5753446.

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ACCESSION AP008278 1 GI:3067387
VERSION AP008278 1
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 3089)
AUTHORS Johnson, G.L.
TITLE Mitogen ERK kinase kinase (MEKK) assay
JOURNAL Patent: US 5753446-A 5 19-MAY-1998;
FEATURES
BASE COUNT 752 a 839 c 871 g 627 t
ORIGIN
Query Match 4.1%; Score 73; DB 6; Length 3089;
Best Local Similarity 100.0%; Pred. No. 1.4e-30;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCTGAGCTCCACCGGGTGGGGGCTCTAGAACTAGTGGATCCCGGGGTTGCGAGG 60
DB 11 AGCTGAGCTCCACCGGGTGGGGGCTCTAGAACTAGTGGATCCCGGGGTTGCGAGG 70
QY 61 AATTCGGCAGCAG 73
DB 71 AATTCGGCAGCAG 83

RESULT 39
AP068732
LOCUS AP068732 3089 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 5 from patent US 5854043.
ACCESSION AP068732
VERSION AP068732 1 GI:6000939
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 3089)
AUTHORS Johnson, G.L.
TITLE MEKK-related signal transduction kinases
JOURNAL Patent: US 5854043-A 5 29-DEC-1998;
FEATURES
BASE COUNT 752 a 839 c 871 g 627 t
ORIGIN
Query Match 4.1%; Score 73; DB 6; Length 3089;
Best Local Similarity 100.0%; Pred. No. 1.4e-30;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCTGAGCTCCACCGGGTGGGGGCTCTAGAACTAGTGGATCCCGGGGTTGCGAGG 60
DB 11 AGCTGAGCTCCACCGGGTGGGGGCTCTAGAACTAGTGGATCCCGGGGTTGCGAGG 70
QY 61 AATTCGGCAGCAG 73
DB 71 AATTCGGCAGCAG 83

RESULT 40
AP085074
LOCUS AP085074 3089 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 5 from patent US 5981265.
ACCESSION AP085074
VERSION AP085074.1 GI:10011845
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 3089)

```

AUTHORS Johnson, G.L.
 TITLE Methods for regulating MEKK protein activity
 JOURNAL Patent: US 5981265-A 5 09-NOV-1999;
 FEATURES Location/Qualifiers
 source 1..3089

BASE COUNT 752 a 839 c 871 g 627 t
 ORIGIN

Query Match 4.1% Score 73; DB 6; Length 3089.

Best Local Similarity 100.0%; Pred. No. 1.4e-30; Mismatches 0; Indels 0; Gaps 0;
 Matches 73; Conservative 0

QY 1 AGCTGGAGCTTCACCGGCGGCTGCTAGAACTAGTGGATCGGCGGCGGCTGGAGG 60
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 Db 11 AGCTGGAGCTTCACCGGCGGCTGCTAGAACTAGTGGATCGGCGGCGGCTGGAGG 70

QY 61 AATTCGGCAGGAG 73
 ||||||||||||

Db 71 AATTCGGCAGGAG 83

RESULT 41

LOCUS AR098267 3089 bp DNA linear PAT 14-FEB-2001
 DEFINITION Sequence 5 from patent US 6074861.
 ACCESSION AR098267
 VERSION AR098267.1 GI:12807524
 KEYWORDS Unknwn.
 SOURCE Unknwn.
 ORGANISM Unknwn.

REFERENCE 1 (bases 1 to 3089)
 AUTHORS Johnson, G.L.
 TITLE MEKK proteins
 JOURNAL Patent: US 6074861-A 5 13-MAY-2000;
 FEATURES Location/Qualifiers
 source 1..3089

BASE COUNT 752 a 839 c 871 g 627 t
 ORIGIN

Query Match 4.1% Score 73; DB 6; Length 3089.

Best Local Similarity 100.0%; Pred. No. 1.4e-30; Mismatches 0; Indels 0; Gaps 0;
 Matches 73; Conservative 0

QY 1 AGCTGGAGCTTCACCGGCGGCTGCTAGAACTAGTGGATCGGCGGCGGCTGGAGG 60
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 Db 11 AGCTGGAGCTTCACCGGCGGCTGCTAGAACTAGTGGATCGGCGGCGGCTGGAGG 70

QY 61 AATTCGGCAGGAG 73
 ||||||||||||

Db 71 AATTCGGCAGGAG 83

RESULT 42

LOCUS AP181005 3089 bp DNA linear PAT 20-APR-2002
 DEFINITION Sequence 9 from patent US 6333170.
 ACCESSION AP181005
 VERSION AP181005.1 GI:20223038
 KEYWORDS Unknwn.
 SOURCE Unknwn.
 ORGANISM Unknwn.

REFERENCE 1 (bases 1 to 3089)
 AUTHORS Johnson, G.L.
 TITLE Method and product for regulating cell responsiveness to external
 signals
 JOURNAL Patent: US 6333170-A 9 25-DEC-2001;
 FEATURES Location/Qualifiers
 source 1..3089

BASE COUNT 752 a 839 c 871 g 627 t
 ORIGIN

BASE COUNT 752 a 839 c 871 g 627 t
 ORIGIN

Query Match 4.1% Score 73; DB 6; Length 3089;

Best Local Similarity 100.0%; Pred. No. 1.4e-30; Mismatches 0; Indels 0; Gaps 0;
 Matches 73; Conservative 0

QY 1 AGCTGGAGCTTCACCGGCGGCTGCTAGAACTAGTGGATCGGCGGCGGCTGGAGG 60
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 Db 11 AGCTGGAGCTTCACCGGCGGCTGCTAGAACTAGTGGATCGGCGGCGGCTGGAGG 70

QY 61 AATTCGGCAGGAG 73
 ||||||||||||

Db 71 AATTCGGCAGGAG 83

RESULT 43

LOCUS AR164434 3328 bp DNA linear PAT 17-OCT-2001
 DEFINITION Sequence 1 from patent US 6271443.
 ACCESSION AR164434
 VERSION AR164434.1 GI:16235654
 KEYWORDS Unknwn.
 SOURCE Unknwn.
 ORGANISM Unknwn.

REFERENCE 1 (bases 1 to 3328)
 AUTHORS Stalker, D.M., Pear, J.P., and Delmer, D.
 TITLE Cotton and rice cellulose synthase DNA sequences
 JOURNAL Patent: US 6271443-A 1 07-AUG-2001;
 FEATURES Location/Qualifiers
 source 1..3328

BASE COUNT 314 a 589 c 763 g 462 t
 ORIGIN

Query Match 4.1% Score 73; DB 6; Length 3328.

Best Local Similarity 100.0%; Pred. No. 1.5e-30; Mismatches 0; Indels 0; Gaps 0;
 Matches 73; Conservative 0

QY 1 AGCTGGAGCTTCACCGGCGGCTGCTAGAACTAGTGGATCGGCGGCGGCTGGAGG 60
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 Db 30 AGCTGGAGCTTCACCGGCGGCTGCTAGAACTAGTGGATCGGCGGCGGCTGGAGG 89

QY 61 AATTCGGCAGGAG 73
 ||||||||||||

Db 90 AATTCGGCAGGAG 102

RESULT 44

LOCUS AX451799 3513 bp DNA linear PAT 03-JUL-2002
 DEFINITION Sequence 7 from Patent WO0238803.
 ACCESSION AX451799
 VERSION AX451799.1 GI:21698666
 KEYWORDS human.
 SOURCE Homo sapiens

REFERENCE 1
 AUTHORS Eichmueller, S., Schadendorf, D. and Usener, D.
 TITLE Novel marker for the diagnosis and therapy of tumours
 JOURNAL Patent: WO 0238803-A 7 16-MAY-2002;
 DEUTSCHES KREBSFORSCHUNGSZENTRUM STIFTUNG DES OEFFENTLICHEN RECHTS
 (DE)

BASE COUNT 1234 a 723 c 867 g 589 t
 ORIGIN

FEATURES Location/Qualifiers
 source 1..3513
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

100

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OM nucleic - nucleic search, using sw model

Run on: October 31, 2002, 10:08:50 : Search time 1991 Seconds
(without alignments)
14430.333 Million cell updates/sec

Title: US-09-854-300-7

Perfect score: 1774

Sequence: 1 agctggagctccaccaggt..... atagggaagttctctctcag 1774

Scoring table: OLIGO-NUC

Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308172

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database :

EST:*

1: em_estba:*
2: em_esthm:*
3: em_estln:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_btc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_othr:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	591	33.3	1954 11	BC030951 Homo sapi
2	491	27.7	557 13	BM527037 Hs21a2c1y
3	484	27.3	1806 11	BC012931 Homo sapi
4	446	25.1	876 10	AF560200 AV86b169
5	446	25.1	683 10	AV86b169 AV86b169
6	418	23.6	602 12	RG155006 RG155006

7	409	23.1	841	12	BF696359
8	409	23.1	847	12	BE958515
9	395	22.3	683	10	AV692456
10	388	21.9	774	12	BG432146
11	384	21.6	841	12	BF666880
12	376	21.2	811	13	BE600046
13	374	21.1	856	12	BE958087
14	359	20.2	884	12	BF542034
15	349	19.7	879	12	BF666897
16	349	19.7	1000	13	BI600419
17	343	19.3	862	12	BF700761
18	340	19.2	906	12	BG165370
19	329	18.5	773	13	BI601096
20	322	18.2	759	12	BE958295
21	300	16.9	863	12	BF697105
22	298	16.8	872	12	BF699229
23	295	16.6	466	12	BF382058
24	294	16.6	759	12	BG400279
25	287	16.2	482	13	BI715115
26	280	15.8	835	12	BE958350
27	256	14.4	458	14	H48650
28	240	13.5	862	12	BF668554
29	238	13.4	818	12	BF698503
30	228	12.9	854	12	BF670202
31	227	12.8	545	13	BI964160
32	224	12.6	358	14	T50929
33	223	12.6	619	13	BG991456
34	221	12.5	732	12	BF246687
35	220	12.4	400	14	D60241
36	220	12.4	876	12	BF665797
37	214	12.1	807	12	BF701837
38	214	12.1	938	12	BF698234
39	193	10.9	1150	13	BI488609
40	187	10.5	593	12	BE959288
41	186	10.5	693	12	BF696365
42	179	10.1	462	10	AW583705
43	176	9.9	368	14	R24902
44	163	9.2	561	12	BE958612
45	163	9.2	855	12	BF666952
46	161	9.1	234	14	CI5261
47	158	8.9	904	12	BF664617
48	150	8.5	445	10	BE536963
49	145	8.2	769	12	BF032034
50	135	7.6	304	13	BG960989
51	130	7.3	896	12	BF665003
52	127	7.2	562	12	BF131792
53	125	7.0	942	12	BF967109
54	122	6.9	789	12	BF669635
55	109	6.1	718	12	BF029934
56	106	6.0	534	12	BF695871
57	104	5.9	784	12	BF700216
58	96	5.4	160	9	AA155685
59	94	5.3	227	14	D81750
60	87	4.9	239	14	BQ352573
61	83	4.7	635	12	BF698021
62	83	4.7	676	12	BF697847
63	82	4.7	770	12	BF700926
64	82	4.6	244	14	CI5568
65	80	4.5	1067	13	BM460110
66	79	4.5	801	10	BE421538
67	79	4.5	846	12	BF695972
68	78	4.4	575	10	AW914131
69	77	4.3	149	10	AW914243
70	77	4.3	202	10	AW914219
71	77	4.3	525	14	BQ078956
72	77	4.3	533	14	BQ078957
73	77	4.3	535	10	AW914117
74	77	4.3	652	10	AW913953
75	77	4.3	854	10	BE414171

ALIGNMENTS

RESULT 1

BC030951 1554 bp mRNA linear HTC 13-JUN-2002
 LOCUS Homo sapiens, hypothetical protein FLJ23516, clone IMAGE4280352,
 DEFINITION mRNA.

ACCESSION

BC030951

VERSION

BC030951.1 GI:21410654

KEYWORDS

HTC.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1554).

Strausberg, R.

Direct Submission

Submitted (03-JUN-2002) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: CLONTECH Laboratories, Inc.

DNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)

Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www.sbc.stanford.edu>

Contact: (Dickson, Mark) mdickson@stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,

R. M.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium URL at <http://imgc-101.g-w>

Series: IRAL Plate: 41 Row: C Column: 10

This clone was selected for full length sequencing because it

passed the following selection criteria: matched mRNA gi: 13375696

This clone has the following problem: frame shifted.

Location/Qualifiers

1..1554

/organism="Homo sapiens"

/db_xref="LocusID:79589"

/db_xref="taxon:9606"

/clone="IMAGE:4280352"

/tissue_type="Brain, primitive neuroectodermal"

/clone_lib="NIH_MGC_56"

/lab_host="DH10B"

/note="Vector: pDNR-LIB"

BASE COUNT 676 a 294 c 346 g 638 t

ORIGIN

Query Match 33.3% Score 591; DB 11; Length 1954;

Best Local Similarity 99.5%; Pred. No. 0;

Matches 791; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 900 TGTCTTTTATTATTAGGAGGCAACTGAGGATATTATCTTTTATCTCTCAAA 959

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Db 1 TGTCTTTTATTATTAGGAGGCAACTGAGGATATTATCTTTTATCTCTCAAA 60

|||||

QY 960 GGTACGGAATCAAGAGCTCAAGCAGGAGCAGGAGCAATTAAGGCGAGATCTAAAA 1019

|||||

Db 61 GGTACGGAATCAAGAGCTCAAGCAGGAGCAGGAGCAATTAAGGCGAGATCTAAAA 120

|||||

QY 1020 AAGCATTTGAAAGGTTCAACTAGCACTACTAAACAGAGGAGCAAGGAAATTTGCTG 1079

|||||

Db 121 AAGCATTTGAAAGGTTCAACTAGCACTACTAAACAGAGGAGCAAGGAAATTTGCTG 180

|||||

QY 1080 ATGAGATAGCTTGTGTGTGTCATGATTTGATTAACCAATGATTTGCTGATCT 1139

|||||

Db 181 ATGAGATAGCTTGTGTGTGTCATGATTTGATTAACCAATGATTTGCTGATCT 240

|||||

QY 1140 TAAAGTTCATATTTCATAGATATGTGTTGATGATGATGATGATGATGATGATG 1199

Db 241 TAACTGCAACCATATTTTCCATAGACATGTGTGACCCATGCTTTAGACACAGGA 300
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 QY 1200 CTTGCCCATCTGCAAAATGTGACATACCTCAAGGCTTTGGGAATTTGAGTGTGTAAG 1259
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 Db 301 CTTGCCCATCTGCAAAATGTGACATACCTCAAGGCTTTGGGAATTTGAGTGTGTAAG 360
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 QY 1250 ATGAGATAGCTTGTGTGTGTCATGATTTGATTAACCAATGATTTGCTGATCT 1319
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 Db 361 ATGAGATAGCTTGTGTGTGTCATGATTTGATTAACCAATGATTTGCTGATCT 420
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 QY 1320 ATGAGATAGCTTGTGTGTGTCATGATTTGATTAACCAATGATTTGCTGATCT 1379
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 Db 421 ATGAGATAGCTTGTGTGTGTCATGATTTGATTAACCAATGATTTGCTGATCT 480
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 QY 1380 ATGAGATAGCTTGTGTGTGTCATGATTTGATTAACCAATGATTTGCTGATCT 1439
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 Db 481 ATGAGATAGCTTGTGTGTGTCATGATTTGATTAACCAATGATTTGCTGATCT 540
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 QY 1440 ATGAGATAGCTTGTGTGTGTCATGATTTGATTAACCAATGATTTGCTGATCT 1499
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 Db 541 ATGAGATAGCTTGTGTGTGTCATGATTTGATTAACCAATGATTTGCTGATCT 600
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 QY 1500 ATGAGATAGCTTGTGTGTGTCATGATTTGATTAACCAATGATTTGCTGATCT 1559
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 Db 601 ATGAGATAGCTTGTGTGTGTCATGATTTGATTAACCAATGATTTGCTGATCT 660
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 QY 1560 ATGAGATAGCTTGTGTGTGTCATGATTTGATTAACCAATGATTTGCTGATCT 1619
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 Db 661 ATGAGATAGCTTGTGTGTGTCATGATTTGATTAACCAATGATTTGCTGATCT 720
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 QY 1620 ATGAGATAGCTTGTGTGTGTCATGATTTGATTAACCAATGATTTGCTGATCT 1679
 |||||
 Db 721 ATGAGATAGCTTGTGTGTGTCATGATTTGATTAACCAATGATTTGCTGATCT 780
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 QY 1680 ATGAGATAGCTTGTGTGTGTCATGATTTGATTAACCAATGATTTGCTGATCT 1694
 |||||
 Db 781 ATGAGATAGCTTGTGTGTGTCATGATTTGATTAACCAATGATTTGCTGATCT 795
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FEATURES

source

BM507037 557 bp mRNA linear EST 15-FEB-2002
 ih24a05.y1 Human insulinoma Homo sapiens cDNA 5' similar to
 TR:Q9ULK6 Q9ULK6 KIAA1214 PROTEIN ; mRNA sequence.

ACCESSION BM507037
 VERSION BM507037.1 GI:18678180
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 557)

Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,

Lemishka, T., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,

Hillier, L., Marra, M., Pape, D., Wyllie, T., Martin, J., Blais, A.,

Schmitt, A., Theisling, B., Rittner, E., Ronko, L., Bennett, J., Cardenas,

M., Gibbons, M., McCann, P., Cole, P., Tsagareishvili, P., Williams, T.,

Jackson, Y. and Bowers, Y.

Endocrine Pancreas Consortium

Unpublished (2000)

Other ESTs: ih24a05.x1

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,

MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@bioh.harvard.edu

Library was constructed by Dr. J. Ferrer In vivo mass-excised to

pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington

University Genome Sequencing Center For information on obtaining a

```

IMAGE:4456033, mRNA.
ACCESSION      BC012931
VERSION        BC012931.1  GI:15277870
KEYWORDS       HTC.
SOURCE         Homo sapiens.
ORGANISM       Homo sapiens.
REFERENCE      Submitted (20-AUG-2001) National Institutes of Health, Mammalian
AUTHORS        Gene Collection (MGC), Cancer Genomics Office, National Cancer
TITLE           Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
JOURNAL        USA
PEMARK         NIH-MGC Project URL: http://mgc.ncbi.nih.gov
COMMENT        Contact: MGC help desk
                Email: cgapbs.r@mail.nih.gov
                Tissue Procurement: ATCC
                cDNA Library Preparation: Life Technologies, Inc.
                cDNA Library Arrayed by: The I M A G.E. Consortium (LMNL)
                DNA Sequencing by: Baylor College of Medicine Human Genome
                Sequencing Center
                Center code: BCM-HGSC

```

```
Center code: BCM-HGSC  
Web site: http://www.hgsc.bcm.tmc.edu/cdna/  
Contact: villalon@bcm.tmc.edu.  
Villalon, D.K., Luna, P.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,  
A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,  
Muzny,D.M., Gibbs,R.A.
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E Consortium/LIML at: http://image.llnl.gov Series: iFAK Plate: 28 Row: G Column: 9 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA yf..10440232

This clone has the following problem: incomplete processing.

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FEATURES             Location/Qualifiers
     source            1..1806
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4456033"
                     /tissue-type="Kidney, hypernephroma"
                     /clone_lib="NIH_MGC_89"
                     /lab_host="DH10B"
                     /note="Vector: pCMW-SPORT6"
BASE COUNT          616 a   266 c   317 g    607 t
ORIGIN
Query Match         27.3% Score 484, DB 11 Length 1806;
Best Local Similarity 99.5%; Pred.No. 6.9e-262;
Matches 634, Conservative 0, Mismatches 3; Indels 0; Gaps 0;
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QY 1058 GSACAGAAGAAATTGGCCCTGATCGAGTAGTGTGTCGTGTCGATGTGAATTTGTATAAA 1117

Dub 1 GSACAGAAGAAATTGGCCCTGATGAGAGTAGTGTCGTGTCGATGTGAATTTGTATAAA 60

QY 1118 CCAATCATTTGGTAGCACCATTTAAGCGTCAACACCATTATTTCCATAAGACATGTGTTGAC 1177

Dub 61 CCAAATCATTTGGTAGCACCATTTAAGCGTCAACACCATTATTTCCATAAGACATGTGTTGAC 120

QY 1178 CCATGCCCTGTIAAACACAAGACTTCCCACATGTCCAATGTGCATCTACATCAAGCTTTC 1237

Td 1 CCATGSG-TSTTAAA-AAGAG-CATGCCCCATGTCAAAATGTGACATACTCAAGGTTTTG 189

QY 1238 GGAAATTTCAGTGTGATGTTTAAAGATGSATCASPTSTCTTTTACAAGTCCCTGTSTATCSAATGAA 1297

Dub 181 GGAAATTAAGSIGSATGTTTAAAGATGSAAT-ASGTGTCCTTTACAAGTCCCTGTATCCAATGAA 240

QY 1298 ATATCTAATAGTCCTTCCTCCCATGAAGAGGTAATATCCAGCGAGACGGCATCATCTGGA 1357

Dub 241 ATATCTAATAGTCCTTCCTCCCATGAAGAGGTAATATCCAGCGAGACGGCATCATCTGGA 300

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[illegible]

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Db 301 TATGTTTCACTATAGGTAATAGATGAACGGCTCTGGAGAACAGTGCAGTCAACAAT 360
Qy 1418 GAAGTGTACAGTGGTAAACCATGAAGCAAAATTTGTGGCAGTGGATTTATCTCAT 1477
Db 361 GAAAGTGTACAGTGGTAAACCATGAAGCAAAATTTGTGGCAGTGGATTTATCTCAT 420
Qy 1478 GTNGACACCCCAACCTTTGAAGAGAGACGAAACTCCTAATCAAGAGACTGCTCTTCGAGAA 1537
Db 421 GTTGACACCCCAACCTTTGAAGAGAGACGAAACTCCTAATCAAGAGACTGCTCTTCGAGAA 480
Qy 1538 ATTAATCTTTAAATCTGTGTAATAATAGAAAACCTTTGAACCATTTAGTAATAACAGAACTGCC 1597
Db 481 ATTAATCTTTAAATCTGTGTAATAATAGAAAACCTTTGAACCATTTAGTAATAACAGAACTGCC 540
Qy 1598 AATCAGGCTAGTCTTCTATTATAAATTTGGATAAAATTTAATAAATAGAGTATACG 1657
Db 541 AATCAGGCTAGTCTTCTATTATAAATTTGGATAAAATTTAATAAATAGAGTATACG 600
Qy 1658 AAGTGTCTAGACTAATATTATGCTATAGTTAA 1694
Db 601 AAGTGTCTAGACTAATATTATGCTATAGTTAA 637

RESULT 4
AV690200 676 bp mpna linear EST 16-JAN-2002
LOCUS AV690200 GKC Homo sapiens cDNA clone GKCA02 5', mpna sequence.
DEFINITION AV690200
ACCESSION AV690200
VERSION AV690200.1 GI:10292063
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
Hu,G., Gu,J., Chen,Z., and Han,Z.
TITLE Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
MEDLINE 21625106
COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@hgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES
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XhoI"
BASE COUNT 94 a 223 c 231 g 125 t 3 others
ORIGIN
Query Match 25.1% Score 446 Db 10 Length 676;
Best Local Similarity 100.0% Pred. No. 2,1e-240; Indels 0 Gaps 0;
Matches 446 Conservative 0 Mismatches 0
Qy 74 GAGAGAGTCTATTTGGTGAATTTGTGTAAGTATGCTCTCTGTAAGT 133
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Db 4 CCGAGGAGCTGCATCTGGCGCAACCTGTGTGCTGACGTACGTGCTCTCGCTCCGACG 63
Qy 134 TAGCTCGCAGCTCCCGAGTCTCACTCCATTCTCTCCACCTGGCGGCACCTGCTCAAG 193
|||||
Db 64 TAGCTCGCAGCTCCCGAGTCTCACTCCATTCTCTCCACCTGGCGGCACCTGCTCAAG 123
Qy 194 ACCAGGCTCTCTGCAAGCGCTAGGAGGCGCTGCAGGGGCGCTAGGGAACCTGGGAGC 253
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Db 124 ACCAGGCTCTCTGCAAGCGCTAGGAGGCGCTGCAGGGGCGCTAGGGAACCTGGGAGC 183
Qy 254 GCCTGGCCCATGAGGGCCCGCCCTGGGGCCGGGGTCTCTCTCCCGGGTGGGTGGGGCTTT 313
|||||
Db 184 GCCTGGCCCATGAGGGCCCGCCCTGGGGCCGGGGTCTCTCTCCCGGGTGGGTGGGGCTTT 243
Qy 314 TCCAGATTGCTGCATGGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 373
|||||
Db 244 TCCAGATTGCTGCATGGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 303
Qy 374 GGGGCTGAAGCAGTGTGGACCGCTACCTCAACGTTCTCTCTCTCTCTCTCTCTCTCTCT 433
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Db 304 GGGGCTGAAGCAGTGTGGACCGCTACCTCAACGTTCTCTCTCTCTCTCTCTCTCTCTCT 363
Qy 434 GTCAACCGTACGCTGTGGAGCGTGGAGGAGGCGGTGTACGGCCAGGACTCGCCGCTG 493
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Db 364 GTCAACCGTACGCTGTGGAGCGTGGAGGAGGCGGTGTACGGCCAGGACTCGCCGCTG 423
Qy 494 GAGCTGTGCTGGTGGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 519
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Db 424 GAGCTGTGCTGGTGGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 449

RESULT 5
AV686169 683 bp mpna linear EST 16-JAN-2002
LOCUS AV686169 GKC Homo sapiens cDNA clone GKCA1E10 5', mRNA sequence.
DEFINITION AV686169
ACCESSION AV686169
VERSION AV686169.1 GI:10288032
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
Hu,G., Gu,J., Chen,Z., and Han,Z.
TITLE Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
MEDLINE 21625106
COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@hgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES
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/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
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BASE COUNT 98 a 222 c 238 g 135 t
ORIGIN

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/Note="Organ: kidney; Vector: pCMV-SPORT6; Site.1: NotI;
Site.2: SalI. Cloned unidirectionally, oligo-dT primed.
Average insert size 1.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC library."

BASE COUNT      294 a      151 c      172 g      284 t
ORIGIN

Query Match      23.6%; Score 418; DB 12; Length 902;
Best Local Similarity 99.8%; Pred. No. 1.5e-224;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1226 CTCAAAGCTTTGGGAATTTGAGTGGATGTTCAAGATGGATGATGCTCTTTTACAAGTCCCT 1285
Db 1 CTCAAAGCTTTGGGAATTTGAGTGGATGTTCAAGATGGATGATGCTCTTTTACAAGTCCCT 60

QY 1286 GTATCCATGAATATCTAATAGTGCCTCTCCCATGAAGAGATATCCGACGAGACC 1345
Db 61 GTATCCATGAATATCTAATAGTGCCTCTCCCATGAAGAGATATCCGACGAGACC 120

QY 1346 GCATCATCTGGATATGCTTCAGTACAGGGAACAGATGAACCCGCTCTGGAGGAACACGTG 1405
Db 121 GCATCATCTGGATATGCTTCAGTACAGGGAACAGATGAACCCGCTCTGGAGGAACACGTG 180

QY 1406 CAGTCAACAAATGAAGTCTACAGCTGGTAAACCATGAAGCAAAATCTCTGGCAGTGGAT 1465
Db 181 CAGTCAACAAATGAAGTCTACAGCTGGTAAACCATGAAGCAAAATCTCTGGCAGTGGAT 240

QY 1466 GTTATTCCTCATGTCAGCAACCCCAACCTTTGAAGAGACCAAACTCCTATCAAGAGACT 1525
Db 241 GTTATTCCTCATGTCAGCAACCCCAACCTTTGAAGAGACCAAACTCCTATCAAGAGACT 300

QY 1526 GCTGTTCGAGAAATTAATCTTAAATCTGTGTAATAGAAAACTTGAACCATTAGTAAT 1585
Db 301 GCTGTTCGAGAAATTAATCTTAAATCTGTGTAATAGAAAACTTGAACCATTAGTAAT 360

QY 1586 AACAGAACTGCCATCAGGCGCTAGTTTCTATTAAATTAATGATTAATTAATAAATA 1645
Db 361 AACAGAACTGCCATCAGGCGCTAGTTTCTATTAAATTAATGATTAATTAATAAATA 420

QY 1646 AGAGTGATCTGAAAGTGCCTCAGATGACTAATATTATGCTATAGTTAA 1694
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RESULT 7
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LOCUS        631124211.F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:428562 5',
DEFINITION   mRNA sequence.
ACCESSION    BF696359
VERSION      BF696359.1 GI:11981767
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 841)
AUTHORS     NIH-MGC http://mgi.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: ATCC
              cDNA Library Preparation: Life Technologies, Inc.
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I M A G E Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLAM10245 row: g column: 17
              High quality sequence stop: 710.
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                  /tissue_type="hypernephroma, cell line"
                  /lab_host="DH10B (phage-resistant)"

FEATURES
source
Location/Qualifiers

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LOCUS AV692456 683 bp mRNA linear EST 16-JAN-2002
 DEFINITION AV692456 GK Homo sapiens cDNA clone GKCCBD09 5', mRNA sequence.
 ACCESSION AV692456
 VERSION AV692456.1 GI:10294319
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 683)
 AUTHORS Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.,
 Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W.,
 Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X.,
 Hu, G., Gu, J., Chen, Z., and Han, Z.
 TITLE Insight into hepatocellular carcinogenesis at transcriptome level
 by comparing gene expression profiles of hepatocellular carcinoma
 with those of corresponding noncancerous liver
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26): 15080-15094 (2001)
 MEDLINE 21625106
 COMMENT Contact: Zenguang Han
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86-21-50801919 (ex. 45)
 Fax: 86-21-50801922
 Email: hanzg@nc.sh.cn
 This clone is available at CHGC in Shanghai.
 FEATURES
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 /clone="GKCCBD09"
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 /lab_host="SOLR"
 /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
 XhoI"
 BASE COUNT 225 a 127 c 126 g 200 t 5 others
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 Best Local Similarity 99.6%; Pred. No. 1 5e-211;
 Matches 495; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1198 GATTGGCCCATGTGTAATGTGACATATCAAAAGCTTTGGGAATGGAGGTGGATGCA 1257
 Db 27 GACTTGGCCCATGTGTAATGTGACATATCAAAAGCTTTGGGAATGGAGGTGGATGCA 86
 QY 1258 AGATGGATCAGTCTTTTACAGTCCCTGTATCCAAATGAAATATCTAATAGTGGCTCC 1317
 Db 87 AGATGGATCAGTCTTTTACAGTCCCTGTATCCAAATGAAATATCTAATAGTGGCTCC 146
 QY 1318 CCATGAAGAGGATATGCGAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1377
 Db 147 CCATGAAGAGGATATGCGAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 296
 QY 1378 AGATGAAGAGGATATGCGAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1437
 Db 207 AGATGAAGAGGATATGCGAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 266
 QY 1438 CCATGAAGAGGATATGCGAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1497
 Db 267 CCATGAAGAGGATATGCGAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 226
 QY 1498 AGAAGAGGAGGATATGCGAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1557
 Db 327 AGAAGAGGAGGATATGCGAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 386
 QY 1558 TAAATGAAGAGGATATGCGAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1617
 Db 387 TAAATGAAGAGGATATGCGAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 446

QY 1618 TAATAAATGGATAAATTTAATAAATAAGAGTGTACTGAAAGTGCTCAGATGACTAAT 1677
 Db 447 TAATAAATGGATAAATTTAATAAATAAGAGTGTACTGAAAGTGCTCAGATGACTAAT 506
 QY 1678 ATTATGCTATAGTAA 1694
 Db 507 ATTATGCTATAGTAA 523
 RESULT 10
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 LOCUS BG432146
 DEFINITION 602496225F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4609831 5',
 mRNA sequence.
 ACCESSION BG432146
 VERSION BG432146.1 GI:13338652
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 774)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 CDNA Library Preparation: CLONTECH Laboratories, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 plate: LLCM1354 row: b column: 08
 High quality sequence stop: 655.
 FEATURES
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 /lab_host="DH10B (T1 phage-resistant)"
 /note="organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
 SfiI (ggcccttcggcc); Site_2: SfiI (ggccattggcc); 5' and
 3' adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCGCGAGCGCGGACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.65
 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC library."
 BASE COUNT 268 a 130 c 140 g 236 t
 ORIGIN
 Query Match 21.9%; Score 388; DB 12; Length 774;
 Best Local Similarity 99.8%; Pred. No. 1 4e-207;
 Matches 438; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1256 GAAGATGGATCAGTGTCTTTACAGTCCCTGTATCCAAATGAAATATCTAATAGTCCCTCC 1315
 Db 1 GAAGATGGATCAGTGTCTTTACAGTCCCTGTATCCAAATGAAATATCTAATAGTCCCTCC 60
 QY 1316 TCCCATGAAGAGGATATGCGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1375
 Db 61 TCCCATGAAGAGGATATGCGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
 QY 1376 ACAGATGAAGCGCTCTGGAGGAGACAGCGAGTGCAGTCAACAAATGAAGTCTACAGCTGGTA 1435
 Db 121 ACAGATGAAGCGCTCTGGAGGAGACAGCGAGTGCAGTCAACAAATGAAGTCTACAGCTGGTA 180
 QY 1436 AACCATGAAGGAAATTTCTGTGGCAGTGTATTTATTTCTCATGTGATGAAATCAACAACTTT 1495

normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

BASE COUNT 153 a 244 c 264 g 150 t
ORIGIN

Query Match 21.2%; Score 376; DB 13; Length 811;
Best Local Similarity 99.6%; Pred. No. 8.7e-201;
Matches 476; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 199 GGTCTCCCAAGCGGTAGCAGCGCGGTGCCAGGCGCGCTAGGAGCACTGGCGAGCGCGG 450
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Db 146 GGTCTCCCAAGCGGTAGCAGGCGCGGTGCCAGGCGCGCTAGGAGCACTGGCGAGCGCGG 205
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QY 259 CGCATGGGCGCGCGCGCGGTGCGCGCGGTCTCTCGCGCGGTGCGCGCGGTCTCTCGAG 318
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Db 206 CGCATGGGCGCGCGCGCGGTGCGCGCGGTCTCTCGCGCGGTGCGCGCGGTCTCTCGAG 265
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QY 319 ATTGCTGGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 378
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QY 379 TGAAGCAGTGTGAGCGCGGTACTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 438
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QY 439 CCGTACGGTGTGGAGCTGAGCGAGGCGGTGTACGGGCTGAGGCTGCGCGGTGTGGAGCG 498
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Db 386 CCGTACGGTGTGGAGCTGAGCGAGGCGGTGTACGGGCTGAGGCTGCGCGGTGTGGAGCG 445
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QY 499 TGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGT 558
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Db 446 TGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGT 505
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QY 559 CAGCAATTTACGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 618
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Db 506 CAGCAATTTACGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 565
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QY 619 CATCCAAACCGCGCGCGCGGTGCGCGGTGCGAGCAAGTCCATCGCTTATGAGAGA 676
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Db 566 CATCCAAACCGCGCGCGCGGTGCGCGGTGCGAGCAAGTCCATCGCTTATGAGAGA 623
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RESULT 13
BE958087
LOCUS 601644929F1 NIH_MGC_56 856 bp mRNA linear EST 04-OCT-2000
DEFINITION BE958087.1 GI:10568792
ACCESSION BE958087
VERSION BE958087.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Sequencing: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM763 row: j column: 07
High quality sequence stop: 635.
Location/Qualifiers

1. .856
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/db_xref="taxon:9606"
/clone="IMAGE:392958"
/clone_lib="NIH_MGC_56"
/tissue_type="primitive neuroectoderm"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ. brain; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggcgctcgcc); Site_2: SfiI (ggcgctcgcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGCCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGCGCGCGCATG-dt(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."

BASE COUNT 305 a 135 c 173 g 243 t
ORIGIN

Query Match 21.1%; Score 374; DB 12; Length 856;
Best Local Similarity 99.8%; Pred. No. 1.2e-199;
Matches 424; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1270 GTCTTTACAGTCCCTGTATCCAAATGAAATATCTAATAGTCCCTCCCATGAAGAGGA 1329
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Db 44 GTCTTTACAGTCCCTGTATCCAAATGAAATATCTAATAGTCCCTCCCATGAAGAGGA 103
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QY 1330 TAATCGCAGGAGACCGCATCATCTGGATATGCTTACAGGAGCAACAGATGAACCGCC 1389
|||||
Db 104 TAATCGCAGGAGACCGCATCATCTGGATATGCTTACAGGAGCAACAGATGAACCGCC 163
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QY 1390 TCTGGAGGAACACGTCAGTCAACAAATGAAAGTCTCAGCTGGTGAACCATGAAGCAAA 1449
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Db 164 TCTGGAGGAACACGTCAGTCAACAAATGAAAGTCTCAGCTGGTGAACCATGAAGCAAA 223
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QY 1450 TTCTTGGCAGTGGATGTTATTCCTCATGTCAGTCAACCAACCTTTGAAGAGCAAGAAC 1509
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Db 224 TTCTTGGCAGTGGATGTTATTCCTCATGTCAGTCAACCAACCTTTGAAGAGCAAGAAC 283
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QY 1510 TCCTTAATCAAGACACTGTGTGTGGAGAAATTAATCTTAAATCTGTGTAATAGAAAC 1569
|||||
Db 284 TCCTTAATCAAGACACTGTGTGTGGAGAAATTAATCTTAAATCTGTGTAATAGAAAC 343
|||||
QY 1570 TTGAACCATTTAGTAATAACAGAACTGCCAATCAGGGCTAGTTTCTATTATTAATTTGA 1629
|||||
Db 344 TTGAACCATTTAGTAATAACAGAACTGCCAATCAGGGCTAGTTTCTATTATTAATTTGA 403
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QY 1630 TAAATTTAATAAATAAGAGTACTGAAAGTCTCAGATGACTATATATGCTATAG 1689
|||||
Db 404 TAAATTTAATAAATAAGAGTACTGAAAGTCTCAGATGACTATATATGCTATAG 463
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QY 1690 TTAATA 1694
|||||
Db 464 TTAATA 468
|||||

RESULT 14
BE9542034
LOCUS 602060189F1 NIH_MGC_58 884 bp mRNA linear EST 11-DEC-2000
DEFINITION BE9542034.1 GI:11629415
ACCESSION BE9542034
VERSION BE9542034.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)


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Db 181 TGACAAACCCACCTTTGAAGAGCGAACTCTCTAATCAGAGACTGCTGTCGAGAAAT 240
QY 1540 TAAATCTTAAATCTGTGTAATAGAAAACCTTGAACCATAGTAATAACAGAACTGCCAA 1599
|||||
Db 241 TAAATCTTAAATCTGTGTAATAGAAAACCTTGAACCATAGTAATAACAGAACTGCCAA 300
QY 1600 TCAGGGCTACTTCTTATTATAATTTGGATAATTTATAATAATAGAGTGTATCTTAA 1659
|||||
Db 301 TCAGGGCTACTTCTTATTATAATTTGGATAATTTATAATAATAGAGTGTATCTTAA 360
QY 1660 AGTGTCTAGTACTAATATTATGCTATAGTTAA 1693
|||||
Db 361 AGTGTCTAGTACTAATATTATGCTATAGTTAA 364

RESULT 18
BG165370 906 bp mRNA linear EST 06-FEB-2001
LOCUS 602346005F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4456033 5',
mRNA sequence.
ACCESSION BG165370
VERSION BG165370.1 GI:12672073
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 906)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10250 row: j column: 02
High quality sequence stop: 649.
Location/Qualifiers
FEATURES
source
1..906
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4456033"
/clone_lib="NIH_MGC_89"
/tissue_type="hypernephroma, cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: kidney; Vector: pCMV-Sport6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT 275 a 204 c 183 g 244 t
ORIGIN
Query Match 19.2%; Score 340; DB 12; Length 906;
Best Local Similarity 99.7%; Pred. No. 2.1e-180;
Matches 390; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1235 TTGGGAATGAGTGGATTTGAAGATGGATAGTGTCTTTTACAGTCCCTGTATCAAT 1294
|||||
Db 175 TTGGGAATGAGTGGATTTGAAGATGGATAGTGTCTTTTACAGTCCCTGTATCAAT 234
QY 1295 GAAATATCTAATAGTGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1364
|||||
Db 235 GAAATATCTAATAGTGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 264
QY 1355 GATATCTCTAGTACTAATATATATATATATATATATATATATATATATATATATAT 1414
|||||

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Db 295 GGATATGCTTCTAGTACAGGGAACAGATGAACCGCTCTTGGAGGAACACGTCAGTCAACA 354
QY 1415 AATGAAGTCTACAGCTGTGAACCATGAAGCAATCTCTGCGACTGGATGTTATCTCT 1474
|||||
Db 355 AATGAAGTCTACAGCTGTGAACCATGAAGCAATCTCTGCGACTGGATGTTATCTCT 414
QY 1475 CATGTGACAAACCAACCTTTGAAGAGAGAGCAAACTCCCTAATCAAGAGACTGCTGTGCA 1534
|||||
Db 415 CATGTGACAAACCAACCTTTGAAGAGAGAGCAAACTCCCTAATCAAGAGACTGCTGTGCA 474
QY 1535 GAAATTAATCTTAAATCTGTGTAATAGAAAACCTTGAACCATAGTAATAACAGAACT 1594
|||||
Db 475 GAAATTAATCTTAAATCTGTGTAATAGAAAACCTTGAACCATAGTAATAACAGAACT 534
QY 1595 GCCAATCAGGGCTAGTCTTCTATTATAAAT 1625
|||||
Db 535 GCCAATCAGGGCTAGTCTTCTATTATAAAT 565

RESULT 19
BG1601096 773 bp mRNA linear EST 07-SEP-2001
LOCUS 603249588F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5301380 5',
mRNA sequence.
ACCESSION BG1601096
VERSION BG1601096.1 GI:15494035
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 773)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11762 row: p column: 21
High quality sequence stop: 759.
Location/Qualifiers
FEATURES
source
1..773
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5301380"
/clone_lib="NIH_MGC_96"
/tissue_type="hypothalamus"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
); oligo-dT primed using primer 5'-TTTTTTTTTTTIVN-3',
size-selected for average insert size 2.3 kb and
normalized to POT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT 130 a 242 c 254 g 146 t
ORIGIN
Query Match 18.5%; Score 329; DB 13; Length 773;
Best Local Similarity 100.0%; Pred. No. 3.5e-174;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 ATTTCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 303
|||||

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(where B = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

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BASE COUNT      289 a   134 c   182 g   258 t
ORIGIN
Query Match      16.9%; Score 300; DB 12; Length 863;
Best Local Similarity 99.7%; Pred. No. 9,1e-158;
Matches 350; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1275 TACAAGTCCTGTATCCATCAATATCTAATAGTGGTCTCCCTCCATCAAGAGGAGATC 1334
Db 1 TACAAGTCCTGTATCCATCAATATCTAATAGTGGTCTCCCTCCATCAAGAGGAGATC 80

QY 1335 GCACGGAGACGGCATCATCTGGGATATGCTTCATAGGAGACATAGAGAGAGAGAGAGAG 1394
Db 61 GCACGGAGACGGCATCATCTGGGATATGCTTCATAGGAGAGAGAGAGAGAGAGAGAGAGAG 120

QY 1395 AGGAGACAGTGCATCAACAAATGAAAGTCTACAGTGTGTAAATCATGAAGTAAATCTGT 1454
Db 121 AGGAGACAGTGCATCAACAAATGAAAGTCTACAGTGTGTAAATCATGAAGTAAATCTGT 180

QY 1455 TGGCAGTGGATCTTATCTCTCATGTGACAAACCAACCTTGAAGAGAGAGAGAGAGAGAG 1514
Db 181 TGGCAGTGGATCTTATCTCTCATGTGACAAACCAACCTTGAAGAGAGAGAGAGAGAGAG 240

QY 1515 ATCAAGACACTGCTGTCGAGAAATTAATCTTAAATCTGTGTAAATGAGAACTTGA 1574
Db 241 ATCAAGACACTGCTGTCGAGAAATTAATCTTAAATCTGTGTAAATGAGAACTTGA 300

QY 1575 CCATTAGTAAATACAGAACTGCCAATCAGGCGCTAGTCTTCTATTATAAAT 1625
Db 301 CCATTAGTAAATACAGAACTGCCAATCAGGCGCTAGTCTTCTATTATAAAT 351

RESULT 22
BF699229 RF699229 872 bp mRNA linear EST 22-DEC-2000
LOCUS 602126878F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4283682 5',
DEFINITION mRNA sequence.
ACCESSION BF699229
VERSION BF699229.1 GI:11984637
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi,
Mammalia; Eutheria; Primates, Catarrhini, Hominidae; Homo.
REFERENCE 1 (bases 1 to 872)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: 602126878 row: 1 column: 19
High quality sequence stop: 588.
Location/Qualifiers
1..872
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4283682"
/clone_lib="NIH_MGC_56"
/tissue_type="primitive neuroectoderm"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1:
source
FEATURES
source 1..872
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4283682"
/clone_lib="NIH_MGC_56"
/tissue_type="primitive neuroectoderm"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1:

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sfII (ggccgctggcc): Site 2: sfII (ggccattatggcc). Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGGCGGCGGACATG-DT(30)BN-3' (where B = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

```

BASE COUNT      276 a   150 c   170 g   246 t
ORIGIN
Query Match      16.8%; Score 298; DB 12; Length 872;
Best Local Similarity 99.7%; Pred. No. 1.2e-156;
Matches 348; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1203 GGGCCATGTGCAATGTGACATACCTCAAGCTTTGGGAATTCAGGTCGATGTTGAAGATG 1262
Db 2 GGGCCATGTGCAATGTGACATACCTCAAGCTTTGGGAATTCAGGTCGATGTTGAAGATG 61

QY 1263 CATCAGTGTCTTTTACAGTCCCTGTATCCCAATCAATATCTAATAGTCCCTGCTCCCATG 1322
Db 62 CATCAGTGTCTTTTACAGTCCCTGTATCCCAATCAATATCTAATAGTCCCTGCTCCCATG 121

QY 1323 AAGAGGATAATCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1382
Db 122 AAGAGGATAATCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 181

QY 1383 AACGGCTCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1442
Db 182 AACGGCTCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 241

QY 1443 AAGCAATCTGTGGCAGTGGATGTTATTCCTCATGTGACAGAGAGAGAGAGAGAGAGAGAG 1502
Db 242 AAGCAATCTGTGGCAGTGGATGTTATTCCTCATGTGACAGAGAGAGAGAGAGAGAGAGAG 301

QY 1503 ACGAACTCTAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1551
Db 302 ACGAACTCTAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 350

RESULT 23
BF382058 RF382058 466 bp mRNA linear EST 27-NOV-2000
LOCUS 601816390F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050022 5',
DEFINITION mRNA sequence.
ACCESSION BF382058
VERSION BF382058.1 GI:11363361
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 466)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC883 row: d column: 23
High quality sequence stop: 466.
Location/Qualifiers
1..466
/organism="Homo sapiens"
/db_xref="taxon:9606"

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/clone="IMAGE:4050022"
 /clone_lib="NIH_MGC_56"
 /tissue_type="primitive neuroectoderm"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1:
 SfiI (ggccgctcgcc); Site_2: SfiI (ggccattatggcc);
 Double-stranded cDNA was prepared from cell line RNA. 5'
 and 3' adaptors were used in cloning as follows: 5'
 adaptor sequence: 5'-CAGGCCATTATGCC-3' and 3' adaptor
 sequence: 5'-ATTCTAGAGGCTGAGCTGCTGAGCAAG-3' (30BP-3',
 where B = A, C, or G and N = A, C, G, or T). Average
 insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
 contained inserts by PCR. This library was enriched for
 full-length clones and was constructed by Clontech
 Laboratories (Palo Alto, CA)."
 BASE COUNT 145 a 92 c 106 g 123 t
 ORIGIN

Query Match 16.6%; Score 295; DB 12; Length 466;
 Best Local Similarity 99.5%; Pred. No. 5.9e-155;
 Matches 395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1083 GAGATAGTGTGCTGTGCTGATGATGATTAACCAAAATGATTTGGTACGCTTTAA 1142
 Db 1 GAGATAGTGTGCTGTGCTGATGATGATTAACCAAAATGATTTGGTACGCTTTAA 60
 QY 1143 CGTCACCATATTTCCATAGACATGCTTTCACCATGCTGCTTTAAACACAACTT 1202
 Db 61 CGTCACCATATTTTCATAGACATGCTTTCACCATGCTGCTTTAAACACAACTT 120
 QY 1203 GCCCATGTGCAATGTGCATATTCACAAATTTTGGCAATGATGATTTGGAAGATG 1262
 Db 121 GCCCATGTGCAATGTGCATATTCACAAATTTTGGCAATGATGATTTGGAAGATG 180
 QY 1263 GATCAGTGTCTTTACAGTCCCTGTATCCAAATGAAATATCTATATGCTCCTCCATC 1322
 Db 181 GATCAGTGTCTTTACAGTCCCTGTATCCAAATGAAATATCTATATGCTCCTCCATC 240
 QY 1323 AAGAGGATAATCGCAGGAGACGCTATCTGATATGTTTACGAGGAGACAGATG 1382
 Db 241 AAGAGGATAATCGCAGGAGACGCTATCTGATATGTTTACGAGGAGACAGATG 300
 QY 1383 AACGCTCTGTGAGACACGCTGACGTCACAAATGAAATGCTACAGCTGGTAAACCAT 1442
 Db 301 AACGCTCTGTGAGACACGCTGACGTCACAAATGAAATGCTACAGCTGGTAAACCAT 360
 QY 1443 AAGCAATCTGTGAGGAGTGTATCTTCTCATGT 1479
 Db 361 AAGCAATCTGTGAGGAGTGTATCTTCTCATGT 397

RESULT 24
 BG400279
 LOCUS 6024647291 NIH_MGC_75 759 bp mRNA linear EST 12-MAR-2001
 DEFINITION mRNA sequence.
 ACCESSION BG400279
 VERSION BG400279.1 GI:13293727
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 759)
 NIH-MGC <http://mgi.nci.nih.gov/>
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT Robert Strausberg, Ph.D.
 Email: cgaps@mail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LCM1331 row: p column: 18
 High quality sequence stop: 736.
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 source
 1. 759
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4592897"
 /clone_lib="NIH_MGC_75"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
 SfiI (ggccgctcgcc); Site_2: SfiI (ggccattatggcc); 5' and
 3' adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-CAGGCCATTATGCC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGGCTGAGCTGCTGAGCAAG-3' (30BP-3', where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.65
 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."
 BASE COUNT 250 a 141 c 141 g 227 t
 ORIGIN

Query Match 16.6%; Score 294; DB 12; Length 759;
 Best Local Similarity 99.7%; Pred. No. 2.3e-154;
 Matches 344; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1224 TACTCAAGCTTTGGCAATGAGTGGATGATTTCAAGATGATGATGCTTTTACAGTCC 1283
 Db 1 TACTCAAGCTTTGGCAATGAGTGGATGATTTCAAGATGATGATGCTTTTACAGTCC 60
 QY 1284 CTGTATCCATGAAATATTAATAGTGGCTCCCATGAGAGGAGATATCCAGCGAGA 1343
 Db 61 CTGTATCCATGAAATATTAATAGTGGCTCCCATGAGAGGAGATATCCAGCGAGA 120
 QY 1344 CCGCATCATCTGGATATGCTTCAGTACAGGAGACACATCAACGCTCTGGAGGAGACAG 1403
 Db 121 CCGCATCATCTGGATATGCTTCAGTACAGGAGACACATCAACGCTCTGGAGGAGACAG 180
 QY 1404 TGCAGTCAACAAATGAAGTCTACAGCTGGTAAACCATGAGCAAAATCTGTGGCAGTGG 1463
 Db 181 TGCAGTCAACAAATGAAGTCTACAGCTGGTAAACCATGAGCAAAATCTGTGGCAGTGG 240
 QY 1464 ATGTTATTCCTCATGTGACACCCCAACCTTTGAAGAGACGAACTCTAATCAAGAGA 1523
 Db 241 ATGTTATTCCTCATGTGACACCCCAACCTTTGAAGAGACGAACTCTAATCAAGAGA 300
 QY 1524 CTGCTGTTGAGAAATTAATCTTAAATCTGTGTAATAGAGAA 1568
 Db 301 CTGCTGTTGAGAAATTAATCTTAAATCTGTGTAATAGAGAA 345

RESULT 25
 BI715115
 LOCUS 1c29p03.y1 HR85 islet Homo sapiens cDNA 5' linear EST 19-SEP-2001
 DEFINITION 1c29p03.y1 HR85 islet Homo sapiens cDNA 5' mRNA sequence.
 ACCESSION BI715115
 VERSION BI715115.1 GI:15690810
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 482)
 Melton, D., Brown, J., Kent, G., Permutt, A., Lee, C., Kaestner, K.,
 Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
 Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,
 Schmitt, A., Theising, B., Ritter, F., Ronko, I., Bennett, J., Cardenas,
 M., Gibbons, M., McCann, R., Cole, R., Tsagarishvili, R., Williams, T.,
 Jackson, Y., and Bowers, Y.
 Endocrine Pancreas Consortium
 TITLE

QY 1339 CGAGACCCGATCATCTGGATATGCTTCAGTACAGGGAACAGATGAACCCCTCTGGAGGA 1398
 Db 61 CGAGACCCGATCATCTGGATATGCTTCAGTACAGGGAACAGATGAACCCCTCTGGAGGA 120
 QY 1399 ACAGCTGCTACACAAATGAAGTCTACAGCTGGTAAACCATGAGCAAAATCTGTGCGC 1458
 Db 121 ACAGCTGCTACACAAATGAAGTCTACAGCTGGTAAACCATGAGCAAAATCTGTGCGC 180
 QY 1459 AGTGGATTTATCTTCATGATGACAAACCAACCTT-1-GAAGAAAGCAAAATCTGTAATC 1517
 Db 181 AGTGGATTTATCTTCATGATGACAAACCAACCTT-1-GAAGAAAGCAAAATCTGTAATC 240
 QY 1518 AAGAGCTGCTGTTCGAGAAATTAATCTTAAATCTGTGTAATAGAAAACCTTGAACCA 1577
 Db 241 AAGAGCTGCTGTTCGAGAAATTAATCTTAAATCTGTGTAATAGAAAACCTTGAACCA 200
 QY 1578 TTACTATAACAGAGTGGCTGATGAGGCTAGTCTTCTTATTAATTAATGCAATTAATTA 1637
 Db 301 TTACTATAACAGAGTGGCTGATGAGGCTAGTCTTCTTATTAATTAATGCAATTAATTA 360
 QY 1638 ATAAATAGAGTGATGATGCTGAAAGTGTCTCAGATGACTAAT 1677
 Db 361 ATAAATAGAGTGATGATGCTGAAAGTGTCTCAGATGACTAAT 400
 RESULT 31
 BI964160 545 bp mRNA linear EST 12-MAR-2002
 LOCUS CDNA clone IMAGE:5671832 5', mRNA sequence.
 ACCESSION BI964160
 VERSION BI964160.1 GI:16338565
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 545)
 Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
 Lemishka, I., Scarce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
 Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,
 Schmitt, A., Theising, B., Ritter, E., Ponko, J., Bennett, J., Cardenas,
 M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, P., Williams, T.,
 Jackson, Y., and Bowers, Y.
 Endocrine Pancreas Consortium
 Published (2000)
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biohpc.harvard.edu
 Library was constructed by Dr. Douglas Melton DNA sequencing by:
 Washington University Genome Sequencing Center For information on
 obtaining a clone please contact: Juliana Brown
 (brownjefas.harvard.edu) This sequence now available from the IMAGE
 Consortium, for clone orders contact: info@image.llnl.gov
 High quality sequence stop: 437.
 Location/Qualifiers
 1..545
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
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 /clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
 /sex="Both"
 /tissue_type="Islets of Langerhans"
 /dev_stage="Adult"
 /lab_host="DH10B"
 /note="Organ: Pancreas; Vector: pSPORT1; Site:1; Not 1;
 Site:2; Sal 1; Starting library constructed using

Superscript Plasmid Library kit (Life Technologies). cDNA made by oligo-dT priming. Size-selected by column fractionation: average insert size 1.08 kb. Library was amplified once on solid support and plasmid DNA from library was prepared. The library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an EcoT of 20. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library.

BASE COUNT 189 a 85 c 83 g 188 t
 ORIGIN
 Query Match 12.8% Score 2271 DB 13 Length 545.
 Best Local Similarity 99.6% Pred. No. 1.8e-116;
 Matches 277; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1417 TGAAGCTCTACAGCTGCTAAACCATGAGCAAAATCTGTGGCAGTGGATGTTATCTCTCA 1476
 Db 1 TGAAGCTCTACAGCTGCTAAACCATGAGCAAAATCTGTGGCAGTGGATGTTATCTCTCA 60
 QY 1477 TGTGACACACCCACCTTTGAAGAGACAGAACTCTTAATCAAGAGACTGCTGTTCGAGA 1536
 Db 61 TGTGACACACCCACCTTTGAAGAGACAGAACTCTTAATCAAGAGACTGCTGTTCGAGA 120
 QY 1537 AATTAATCTTAAATCTGTGTAATAGAAAACCTTGAACCATGTAATTAACAGAACTGC 1596
 Db 121 AATTAATCTTAAATCTGTGTAATAGAAAACCTTGAACCATGTAATTAACAGAACTGC 180
 QY 1597 CAATCAGGCGCTAGTTCCTTATTAAATTTGATGATAATTTAATAAATTAAGAGTGTACT 1656
 Db 181 CAATCAGGCGCTAGTTCCTTATTAAATTTGATGATAATTTAATAAATTAAGAGTGTACT 240
 QY 1657 GAAAGTGCTCAGTCACTACTAATATGCTATAGTTAA 1694
 Db 241 GAAAGTGCTCAGTCACTACTAATATGCTATAGTTAA 278
 T50929 358 bp mRNA linear EST 06-FEB-1995
 YB88E02_r1 Stragatene liver (#937224) Homo sapiens cDNA clone
 IMAGE:78266 5', mRNA sequence.
 T50929 31:652789
 VERSION T50929.1
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 358)
 Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
 Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins,
 M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore,
 B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
 Schellenberg, K., Soares, M.R., Tan, F., Thierri-Meg, J., Trevaskis, E.,
 Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.
 Generation and analysis of 280,000 human expressed sequence tags
 Genome Res. 6 (9), 807-828 (1996)
 9704478
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 High quality sequence stops: 260
 Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: M13Rp1

FEATURES
 source

JOURNAL
COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM927 row: i column: 19
High quality sequence stop: 602.
Location/Qualifiers
1..732
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4075482"
/clone_lib="NIH_MGC_57"
/tissue_type="glioblastoma"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: Brain; Vector: pDRP-LIR (Clontech); Site_1: SfiI (ggcgctcgcc); Site_2: SfiI (ggccattatgcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-ATTCTAGAGCGGCGCCGACATG-dl(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 0.9-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
BASE COUNT 249 a 120 c 139 g 224 t

FEATURES
source

Query Match 12.4% Score 220; DB 14; Length 400;
Best Local Similarity 100.0%; Pred. No. 4.7e-113;
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1255 TGAAGATGGATCAGTCTTTTACAGTCCCTGTATCCCAATGAATATATATAGTGCCTC 1314
Db 11 TGAAGATGGATCAGTCTTTTACAGTCCCTGTATCCCAATGAATATATATAGTGCCTC 70
QY 1315 CTCCTATGAAGAGGATATCGGAGGAGAGCCGCATCATCTGGATATGCTTCAGTACAGGG 1374
Db 71 CTCCTATGAAGAGGATATCGGAGGAGAGCCGCATCATCTGGATATGCTTCAGTACAGGG 130
QY 1375 AATAGATGAACGGCTCTGAGAGAAACACCTGTCAGTCAACAATGAAATGATATATAT 1474
Db 131 AACAGATGAACGGCTCTGAGAGAAACACCTGTCAGTCAACAATGAAATGATATATAT 190
QY 1435 AAACCATGAAGCAAAATCTGTGGCAGTGGATGTTATTCCTC 1475
Db 191 AAACCATGAAGCAAAATCTGTGGCAGTGGATGTTATTCCTC 231

RESULT 35
D60241
LOCUS

DEFINITION HUM093005B Clontech human fetal brain polyA+ mRNA (46535) Homo sapiens cDNA clone GEN-093005 5', mRNA sequence.
VERSION D60241
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS

Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H., Takaichi, A., Takeda, S., Watanabe, T., Takahashi, E., Hirai, Y., Maekawa, H., Shin, S. and Nakamura, Y.
Fujiwara et al. (1995)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 400)
Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M., Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H., Takaichi, A., Takeda, S., Watanabe, T., Takahashi, E., Hirai, Y., Maekawa, H., Shin, S. and Nakamura, Y.
Fujiwara et al. (1995)

TITLE

Unpublished (1995)
Contact: Tsutomu Fujiwara
Otsuka GEN Research Institute
Otsuka Pharmaceutical Co., Ltd
463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima, 771-01 Japan
Tel: 0886-65-2888
Fax: 0886-37-1035.
Location/Qualifiers
1..400
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GEN-093005"
/clone_lib="Clontech human fetal brain polyA+ mRNA (#6535)"
/note="Male adult, hematopoietic tissue, stem cell"
BASE COUNT 146 a 70 c 61 g 123 t

FEATURES
source

Query Match 12.4% Score 220; DB 14; Length 400;
Best Local Similarity 99.6%; Pred. No. 1.6e-112;
Matches 270; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1424 CTACAGCTGGTAAACCATCAAGCAAAATCTGTGGCAGTGGATGTTATTCCTCATGTGAC 1483
Db 8 CTACAGCTGGTAAACCATCAAGCAAAATCTGTGGCAGTGGATGTTATTCCTCATGTGAC 67
QY 1484 AACCCAACTTTGAAGAACGAACTCCTAATCAAGAGACTGCTGTCGAGAAATATAA 1543
Db 68 AACCCAACTTTGAAGAACGAACTCCTAATCAAGAGACTGCTGTCGAGAAATATAA 127
QY 1544 TCTTAAATCTGTGTAATAGAAACTTGACCATTAAGACAGACTGCCAATCAG 1603
Db 128 TCTTAAATCTGTGTAATAGAAACTTGACCATTAAGACAGACTGCCAATCAG 187
QY 1604 GGCTAGTTCCTATTAAATAAATGGATAATTTAATAAATGAAGTACTGAAAGTG 1663
Db 188 GGCTAGTTCCTATTAAATAAATGGATAATTTAATAAATGAAGTACTGAAAGTG 247
QY 1664 CTCAGATGACTAATATTATGCTATAGTTAAA 1694
Db 248 CTCAGATGACTAATATTATGCTATAGTTAAA 278

RESULT 36
BF665797
LOCUS

DEFINITION BF665797 Homo sapiens cDNA clone IMAGE:4381345 5', mRNA sequence.
ACCESSION BF665797.1 GI:11939692
VERSION
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 876)
NIH-MGC http://mgc.ncbi.nlm.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1109 row: k column: 10
High quality sequence stop: 605.
Location/Qualifiers
1..876
/organism="Homo sapiens"

FEATURES
source

Query Match 12.4% Score 220; DB 14; Length 400;
Best Local Similarity 99.6%; Pred. No. 1.6e-112;
Matches 270; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1424 CTACAGCTGGTAAACCATCAAGCAAAATCTGTGGCAGTGGATGTTATTCCTCATGTGAC 1483
Db 8 CTACAGCTGGTAAACCATCAAGCAAAATCTGTGGCAGTGGATGTTATTCCTCATGTGAC 67
QY 1484 AACCCAACTTTGAAGAACGAACTCCTAATCAAGAGACTGCTGTCGAGAAATATAA 1543
Db 68 AACCCAACTTTGAAGAACGAACTCCTAATCAAGAGACTGCTGTCGAGAAATATAA 127
QY 1544 TCTTAAATCTGTGTAATAGAAACTTGACCATTAAGACAGACTGCCAATCAG 1603
Db 128 TCTTAAATCTGTGTAATAGAAACTTGACCATTAAGACAGACTGCCAATCAG 187
QY 1604 GGCTAGTTCCTATTAAATAAATGGATAATTTAATAAATGAAGTACTGAAAGTG 1663
Db 188 GGCTAGTTCCTATTAAATAAATGGATAATTTAATAAATGAAGTACTGAAAGTG 247
QY 1664 CTCAGATGACTAATATTATGCTATAGTTAAA 1694
Db 248 CTCAGATGACTAATATTATGCTATAGTTAAA 278

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/db_xref="taxon:9606"
/clone_image:4281345"
/clone_lib="NIH_MGC_56"
/tissue_type="primitive neuroectoderm"
/lab_host="DH10B (T1 phage-resistant)"
/site_1:
SfiI (ggccctcggcc): Site 2: SfiI (ggccctcggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-ATTTCAGGCGGAGGCGGACATG-dt(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.6 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
BASE COUNT      288 a 140 c 187 g 261 t
ORIGIN

Query Match      12.4% Score 220; DB 12; Length 876;
Best Local Similarity 99.6%; Pred. No. 1.8e-112;
Matches 270; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1389 CTCTGAGGAAACAGTCTATTAACAAATGAAGTCTATATGTTAAAGTATGAAGCAA 1448
DB 89 CTCTGAGGAAACAGTCTATTAACAAATGAAGTCTATATGTTAAAGTATGAAGCAA 148

QY 1449 ATTCTGTGCTAGTCTATATCTCTATGTCAGTATGAGTAAATTAATTTTAAAGTAA 1508
DB 149 ATTCTGTGCTAGTCTATATCTCTATGTCAGTATGAGTAAATTAATTTTAAAGTAA 208

QY 1509 CTCTTAATCAAGCAATCTGTTTGTGAGAAATTAATTTTAAATTTTAAATTAATTA 1568
DB 209 CTCTTAATCAAGCAATCTGTTTGTGAGAAATTAATTTTAAATTTTAAATTAATTA 258

QY 1569 CTCTTAATCAATATATATATATATATATATATATATATATATATATATATATAT 1628
DB 269 CTCTTAATCAATATATATATATATATATATATATATATATATATATATATATAT 328

QY 1629 ATAAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1659
DB 329 ATAAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 359

RESULT 37
BF701837 602128635F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285425 5',
LOCUS mRNA sequence.
DEFINITION EST.
ACCESSION BF701837.1 GI:11987245
VERSION BF701837
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 807)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium, LLC at:
http://image.llnl.gov
Plate: LLCM112 row e column 16
High quality sequence start: 21
High quality sequence stop: 615
High quality sequence stop: 615
Location/Qualifiers

FEATURES
source

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1. 807
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image:4285425"
/clone_lib="NIH_MGC_56"
/tissue_type="primitive neuroectoderm"
/lab_host="DH10B (T1 phage-resistant)"
/site_1:
SfiI (ggccctcggcc): Site 2: SfiI (ggccctcggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-ATTTCAGGCGGAGGCGGACATG-dt(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
BASE COUNT      271 a 152 c 127 g 256 t
ORIGIN

Query Match      12.1% Score 214; DB 12; Length 807;
Best Local Similarity 100.0%; Pred. No. 4.3e-109;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 GATCAATCAAGTCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1540
DB 47 GATCAATCAAGTCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 106

QY 1541 AAATCTTAAATCTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1600
DB 107 AAATCTTAAATCTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 166

QY 1601 CAGGCTCTAGTCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1660
DB 167 CAGGCTCTAGTCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 226

QY 1661 GTCTCTAGTCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1694
DB 227 GTCTCTAGTCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 260

RESULT 38
BF698234 602125574F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4282339 5',
LOCUS mRNA sequence.
DEFINITION EST.
ACCESSION BF698234.1 GI:11983642
VERSION BF698234
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 938)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM112 row d column 29
High quality sequence stop: 604.
High quality sequence stop: 604.
Location/Qualifiers

FEATURES
source

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/clone="IMAGE:4282339"
/clone_lib="NIH_MGC_56"
/tissue_type="primitive neuroectoderm"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggcgctcgcc); Site_2: SfiI (ggcattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCCGAGCGCCGACATG-dt(30)BN-3'
(Where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
BASE COUNT 308 a 189 c 166 g 274 t 1 others
ORIGIN

```

```

Query Match 12.1% Score 214; DB 12; Length 938;
Best Local Similarity 100.0%; Pred. No. 4.4e-109;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 GACAAACCAACCTTTGAAGAGAGCAAACTCTTAATCAAGAGACTGCTGTTCGAGAAAT 1540
Dbb 138 GACAAACCAACCTTTGAAGAGAGCAAACTCTTAATCAAGAGACTGCTGTTCGAGAAAT 197
QY 1541 AATCTTAAATCTGTGTAATAGAAACITGACCAATTAGTATACAGAACTGCCAAT 1600
Dbb 198 AATCTTAAATCTGTGTAATAGAAACITGACCAATTAGTATACAGAACTGCCAAT 257
QY 1601 CAGGCGCTAGTTCTTATTATTAATAATTCGATAAATTTAATAAATAAGACTCATCTGAAA 1660
Dbb 258 CAGGCGCTAGTTCTTATTATTAATAATTCGATAAATTTAATAAATAAGACTCATCTGAAA 317
QY 1641 GTGCTTATATATATATATATATATATATATATATATATATATATATATATATATATAT 1694
Dbb 318 GTGCTTATATATATATATATATATATATATATATATATATATATATATATATATATAT 351

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RESULT 39
LOCUS BI488609 1150 bp mRNA linear EST 28-AUG-2001
DEFINITION 60302137F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5191785 5',
mRNA sequence.
ACCESSION BI488609
VERSION BI488609.1 GI:15327837
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1150)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaaps-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M11479 row: j column: 10
High quality sequence stop: 740.
Location/Qualifiers
1..1150
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5191785"
/clone_lib="NIH_MGC_114"
/lab_host="DH10B"

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FEATURES
source

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/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 019. Note:
this is a NIH_MGC Library."
BASE COUNT 264 a 315 c 336 g 235 t
ORIGIN

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Query Match 10.9% Score 193; DB 13; Length 1150;
Best Local Similarity 99.7%; Pred. No. 3.4e-97;
Matches 313; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 232 GGGCGCTAGGCAACTGGGAGCGCGGCATGGCGCCGCGCGCGCGCGCGCGCGCGCTC 291
Dbb 57 GGGCGCTAGGCAACTGGGAGCGCGGCATGGCGCCGCGCGCGCGCGCGCGCGCGCTC 116
QY 292 CTGCGCGCGGTGGCTGCGCGCTTTTCCAGATTGCTGGCATGCTGCTCTCTGCTGCGCCCTGAG 351
Dbb 117 CTGCGCGCGGTGGCTGCGCGCTTTTCCAGATTGCTGGCATGCTGCTCTCTGCTGCGCCCTGAG 176
QY 352 TCCGAGCAGCACCCGGTTCCCG-GGGGCTGAAGCAGTGTGGACCGGTACCTCAAGCTGT 410
Dbb 177 TCCGAGCAGCACCCGGTTCCCGGTGGGCGCTGAAGCAGTGTGGACCGGTACCTCAAGCTGT 236
QY 411 CCTGCGCGGTTCGCCACACACGGGAGTGAACGCTGCGGAGCTGGGAGCTGAGGAGAGGGCG 470
Dbb 237 CCTGCGCGGTTCGCCACACACGGGAGTGAACGCTGCGGAGCTGGGAGCTGAGGAGAGGGCG 296
QY 471 TGTAGCGCGAGGACTGCGCGCTGGAGCTTGTGCTTGGGCTGCTTACCGCGCGAGTGGG 530
Dbb 297 TGTAGCGCGAGGACTGCGCGCTGGAGCTTGTGCTTGGGCTGCTTACCGCGCGAGTGGG 356
QY 531 CCGGCGCGCTTAAC 544
Dbb 357 CCGGCGCGCTTAAC 370

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RESULT 40
LOCUS BE959288 513 bp mRNA linear EST 04-OCT-2000
DEFINITION 601645341F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930154 5',
mRNA sequence.
ACCESSION BE959288
VERSION BE959288.1 GI:10569993
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 513)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaaps-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M764 row: b column: 11
High quality sequence start: 14
High quality sequence stop: 481.
Location/Qualifiers
1..513
/organism="Homo sapiens"
/db_xref="taxon:9606"

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FEATURES
source

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source
1. .462
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5637219"
/clone_lib="Human Pancreatic Islets"
/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
/notes="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1; Site_2: Sal 1; Library constructed using SuperScript Plasmid Library kit (Life Technologies). cDNA made by oligo-dT priming. Size selected by column fractionation. average insert size 1.08 kb. Primary library, unamplified."
BASE COUNT 139 a 84 c 107 g 130 t 2 others
ORIGIN
Query Match 10 1%; Score 179; DB 10; Length 462;
Best Local Similarity 99.1%; Pred. No. 2.7e-89;
Matches 329; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 852 AAAACATGCGCTTGGGTGAATCATATTCATTTTTCCTGCTGCTTTTAA 911
D 69 AAAACATGCGCTTGGGTGAATCATATTCATTTTTCCTGCTGCTTTTAA 128
QY 912 TTATACGGGCAACTGTGGGTATTTATCTTTTATCTGCTGAGGCTACGATG 971
D 129 TTATACGGGCAACTGTGGGTATTTATCTTTTATCTGCTGAGGCTACGATG 188
QY 972 CAAGAGCTCAAGCAGGAGGCAATTAAGGCGAGATCTAAAGAACTATTGAA 1031
D 189 CAGAGCTCAAGCAGGAGGCAATTAAGGCGAGATCTAAAGAACTATTGAA 248
QY 1032 GGCTTCAACTACGACACTGAACAGGAGGCAAGAAATGGCCCTGATGGAGATGT 1091
D 249 GGCTTCAACTACGACACTGAACAGGAGGCAAGAAATGGCCCTGATGGAGATGT 308
QY 1092 GTGCTGTGCTGATTAATGTATTAACCAATGATTTGTGCGGATCTTAAGTGCAC 1151
D 309 GTGCTGTGCTGATTAATGTATTAACCAATGATTTGTGCGGATCTTAAGTGCAC 368
QY 1152 ATATTTCCATAGACATGTGTGACCCATGG 1183
D 369 ATATTTCCATAGACATGTGTGACCCATGG 400

RESULT 43
R24902
LOCUS
DEFINITION
IMAGE:132015 5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
EST.
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 368)
REFERENCE
AUTHORS
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman,
M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Maizumi, M., Parsons, J.,
Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston,
R., Williamson, A., Wohlmann, P. and Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
Insert Size: 1362
High quality sequence stops: 190
Location/Qualifiers

Source
1. .368
/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="GDB:537571"
/db_xref="taxon:9606"
/clone="IMAGE:132015"
/clone_lib="Soares placenta NB2HP"
/sex="Female"
/dev_stage="placenta obtained at birth (full term)"
/lab_host="DH10B (ampicillin resistant)"
/notes="Organ: placenta; Vector: pT73D (Pharmacia) with a modified Polylinker, Site_1: Not 1, Site_2: Eco RI, 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' AACTGGAAGAAATCGCGCCGAGGAATTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 107 a 77 c 89 g 95 t
ORIGIN
Query Match 9.9%; Score 176; DB 14; Length 368;
Best Local Similarity 100.0%; Pred. No. 1.3e-87;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1253 GTTGAAGATGGATAGTGTCTTTTACAGTCCCTGTATCCCAATGAAATATCTAATAGTCC 1312
D 1 GTTGAAGATGGATAGTGTCTTTTACAGTCCCTGTATCCCAATGAAATATCTAATAGTCC 60
QY 1313 TCTCTCCATGAGAGATATATCGAGCGAGCCGATCATCTGGATGCTTCAGTACAG 1372
D 61 TCTCTCCATGAGAGATATATCGAGCGAGCCGATCATCTGGATGCTTCAGTACAG 120
QY 1373 GGAACAGATGAACCGCTCTGGAGGAGACACGTGCGAGTCAACAAATGAAAGTCTACA 1428
D 121 GGAACAGATGAACCGCTCTGGAGGAGACACGTGCGAGTCAACAAATGAAAGTCTACA 176

RESULT 44
BE958612
LOCUS
DEFINITION
601645258F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930207 5',
mRNA sequence.
ACCESSION
VERSION
KEYWORDS
EST.
human.
SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 561)
REFERENCE
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM764 row: d column: 16
High quality sequence stops: 560.
Location/Qualifiers

```

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source
1. .561
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:3930207"
/clone_lib="NIH_MGC_56"
/tissue_type="primitive neuroectoderm"
/lab_host="PH10B (T1 phage-resistant)"
/notes="Organ: brain; Vector: pNRR-LIB (Clontech); Site_1: SfiI (ggccattatggcc); Site_2: SfiI (ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-ATTCTAGAGCGGCGGCACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
BASE COUNT 197 a 84 c 86 g 194 t
ORIGIN

Query Match 9.2%; Score 163; DB 12; Length 561;
Best Local Similarity 99.5%; Pred. No. 3.1e-80;
Matches 213; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1481 GACAACCCACCTTTGAGAGAGAGAACTCTTAATCAAGAGACTGCTGTTGAGAAAT 1540
Db 6 GACAACCCACCTTTGAGAGAGAGAACTCTTAATCAAGAGACTGCTGTTGAGAAAT 65

Qy 1541 AAATCTTTAAATCTGTGTAATAAGAAACTTGAACCAATTAGTAATAACAGAACTGCCAAT 1600
Db 66 AAATCTTTAAATCTGTGTAATAAGAAACTTGAACCAATTAGTAATAACAGAACTGCCAAT 125

Qy 1601 CAGGCGCTAGTTCTATTATAATATGGAATAATTTAATAAATAGAGAGTACTGAAA 1660
Db 126 CAGGCGCTAGTTCTATTATAATATGGAATAATTTAATAAATAGAGAGTACTGAAA 185

Qy 1661 GTGCTCAGATGACTAATATTATGCTATAGTTAAA 1694
Db 186 GTGCTCAGATGACTAATATTATGCTATAGTTAAA 219

RESULT 45
BF666952
LOCUS BF666952 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930207, 855 bp mRNA sequence.
DEFINITION BF666952.1 GI:11940847
ACCESSION BF666952
VERSION BF666952.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 855)
NIH-MGC http://imgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph D.
Email: rstrauss@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHCMI102 row: n column: 24
High quality sequence stop: 603.
Location/Qualifiers
1. .855
/organism="Homo sapiens"
/db_xref="taxon:9606"

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/clone="IMAGE:4278743"
/clone_lib="NIH_MGC_56"
/tissue_type="primitive neuroectoderm"
/lab_host="PH10B (T1 phage-resistant)"
/notes="Organ: brain; Vector: pNRR-LIB (Clontech); Site_1: SfiI (ggccattatggcc); Site_2: SfiI (ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-ATTCTAGAGCGGCGGCACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
BASE COUNT 232 a 171 c 168 g 284 t
ORIGIN

Query Match 9.2%; Score 163; DB 12; Length 855;
Best Local Similarity 99.5%; Pred. No. 3.2e-80;
Matches 213; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1481 GACAACCCACCTTTGAGAGAGAGAACTCTTAATCAAGAGACTGCTGTTGAGAAAT 1540
Db 43 GACAACCCACCTTTGAGAGAGAGAACTCTTAATCAAGAGACTGCTGTTGAGAAAT 102

Qy 1541 AAATCTTTAAATCTGTGTAATAAGAAACTTGAACCAATTAGTAATAACAGAACTGCCAAT 1600
Db 103 AAATCTTTAAATCTGTGTAATAAGAAACTTGAACCAATTAGTAATAACAGAACTGCCAAT 162

Qy 1601 CAGGCGCTAGTTCTATTATAATATGGAATAATTTAATAAATAGAGTACTGAAA 1660
Db 163 CAGGCGCTAGTTCTATTATAATATGGAATAATTTAATAAATAGAGTACTGAAA 222

Qy 1661 GTGCTCAGATGACTAATATTATGCTATAGTTAAA 1694
Db 223 GTGCTCAGATGACTAATATTATGCTATAGTTAAA 256

RESULT 46
BF666952
LOCUS BF666952 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278743, 855 bp mRNA sequence.
DEFINITION BF666952.1 GI:11940848
ACCESSION BF666952
VERSION BF666952.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 855)
NIH-MGC http://imgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph D.
Email: rstrauss@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHCMI102 row: n column: 24
High quality sequence stop: 603.
Location/Qualifiers
1. .224
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NIH_MGC_56"
/clone_lib="NIH_MGC_56"
/notes="Male adult, hematopoietic tissue, stem cell"
BASE COUNT 83 a 38 c 37 g 63 t
ORIGIN

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Query Match      9.1%  Score 161; DB 14; Length 224;
Best Local Similarity 100.0%; Pred. No. 3 9e-79;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 GACAAACCAACCTTGAAGAGAGAGAACTCCCTAATCAAGAGACTGCTGTTCAGAAATT 1540
|||||
DB 64 GACAACTCAAGCTTTTGAAGAGAGAGAACTCCCTAATCAAGAGACTGCTGTTCAGAAATT 123
|||||

QY 1541 AAATCTTAAATCTGTGTAAATCAAAACCTTGAACCATTAAGTAAATCAAGAGAGCTGCAAT 1600
|||||
DB 124 AAATCTTAAATCTGTGTAAATCAAAACCTTGAACCATTAAGTAAATCAAGAGAGCTGCAAT 183
|||||

QY 1601 CAGGCGCTAGTTCTTATTAATAATTAATGGATAAATTTAATAA 1641
|||||
DB 184 CAGGCGCTAGTTCTTATTAATAATTAATGGATAAATTTAATAA 224
|||||

RESULT 47
LOCUS      BF664617          904 bp      mRNA      linear      EST 21-DEC-2000
DEFINITION 602117401P1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4274977 5';
mRNA sequence.
ACCESSION  BF664617
VERSION     BF664617.1  GI:11938512
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 904)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgabbs-remail.nih.gov
          Tissue Procurement: ATCC
          cDNA Library Preparation: CLONTECH Laboratories, Inc.
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: L1CMI093 row: b column: 02
          High quality sequence stop: 584.
          Location/Qualifiers
            1..904
              /organism="Homo sapiens"
              /db_xref="taxon:9606"
              /clone_lib="NIH_MGC_56"
              /tissue_type="primitive neuroectoderm"
              /lab_host="DH10B (T1 phage-resistant)"
              /note="Organ: brain; Vector: PNP-LIB (Clontech); Site_1:
              Sf11 (ggccgctggcc); Site_2: Sf11 (ggccattggcc);
              Double-stranded cDNA was prepared from cell line RNA. 5'
              and 3' adaptors were used in cloning as follows: 5'
              adaptor sequence: 5'-CAGGCGCATATGGCC-3' and 3' adaptor
              sequence: 5'-ATTCTAGAGCGGCGGCGACATG-dt(30)BN-3'
              (where B = A, C, or G and N = A, C, G, or T). Average
              insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
              contained inserts by PCR. This library was enriched for
              full-length clones and was constructed by Clontech
              Laboratories (Palo Alto, CA)."
          BASE COUNT  272 a 190 c 195 g 244 t      2 others
          ORIGIN
            1..904
              8.9%  Score 158; DB 12; Length 904;
              Best Local Similarity 100.0%; Pred. No. 2.2e-77;
              Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1032 GGGTTCAACTACGCACTGAAACAAAGGAGACAAAGAAATGGCCCTGATGAGATAGTT 60
|||||
DB 1092 GTCCTGTGTGTAATTTGTAATTAATAACCAATGATTGGTACGATCTTTAAAGCTGCAACC 1151
|||||
DB 61 GTCCTGTGTGTAATTTGTAATTAATAACCAATGATTGGTACGATCTTTAAAGCTGCAACC 120
|||||
QY 1152 ATATTTTCCATAGATATATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1189
|||||
DB 121 ATATTTTCCATAGATATATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 158
|||||

RESULT 48
LOCUS      BE536963          445 bp      mRNA      linear      EST 09-AUG-2000
DEFINITION 601064790F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3450983 5';
mRNA sequence.
ACCESSION  BE536963
VERSION     BE536963.1  GI:9765608
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 445)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgabbs-remail.nih.gov
          Tissue Procurement: ATCC
          cDNA Library Preparation: Life Technologies, Inc.
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM8430 row: d column: 24
          High quality sequence stop: 445.
          Location/Qualifiers
            1..445
              /organism="Homo sapiens"
              /db_xref="taxon:9606"
              /clone_lib="NIH_MGC_10"
              /cell_line="MGC36"
              /lab_host="DH10B"
              /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
              Site_2: Sall; Cloned unidirectionally. Primer: Oligo dt.
              Average insert size 1.5 kb. Library prepared by Life
              Technologies."
          BASE COUNT  152 a 63 c 64 g 166 t
          ORIGIN
            1..445
              8.5%  Score 150; DB 10; Length 445;
              Best Local Similarity 100.0%; Pred. No. 6.9e-73;
              Matches 150; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1545 CTTAAATCTGTCTAATAAGAACTTGAACCATTAAGTAAATCAAGAGACTGCCAATCAGG 1604
|||||
DB 1 CTTAAATCTGTCTAATAAGAACTTGAACCATTAAGTAAATCAAGAGACTGCCAATCAGG 60
|||||
QY 1605 GCCTAGTCTTCTATTAAATTTGGATAAATTTAATAAAAATAGAGTGTACTGAAAGTGC 1664
|||||
DB 61 GCCTAGTCTTCTATTAAATTTGGATAAATTTAATAAAAATAGAGTGTACTGAAAGTGC 120
|||||
QY 1665 TCAGATGACTAATATTATGCTATAGTTAAA 1694
|||||
DB 121 TCAGATGACTAATATTATGCTATAGTTAAA 150
|||||

RESULT 49
LOCUS      BF032034          769 bp      mRNA      linear      EST 10-OCT-2000

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DEFINITION 601559604F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:382297 5',
             mRNA sequence.
ACCESSION  BF032034
VERSION     BF032034.1 GI:10739746
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 769)
AUTHORS     NIH-MGC http://mgc.nhl.nih.gov/
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library: Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone Distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: L10M501 row: h column: 62
            High quality sequence stop: 523.
FEATURES    source
             Location/Qualifiers
               1..769
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone="IMAGE:382297"
               /clone_11b="NIH_MGC_58"
               /tissue_type="hypertrophoma"
               /lab_host="DH10B (TI phage-resistant)"
               /notes="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
               SfiI (ggccgctcgcc); Site_2: SfiI (ggccattggcc);
               Double-stranded cDNA was prepared from cell line RNA. 5'
               and 3' adaptors were used in cloning as follows: 5'
               adaptor sequence: 5'-ATCTAGAGCGGCGGCGGCGCATG-dr(30)BN-3'
               (where B = A, C, or G and N = A, C, G, or T). Average
               insert size 1.35 kb (range 0.9-4.0 kb). 15/15 colonies
               contained inserts by PCR. This library was enriched for
               full-length clones and was constructed by Clontech
               Laboratories (Palo Alto, CA)."
BASE COUNT  236 a 164 c 127 g 242 t
ORIGIN
Query Match      8.2%; Score 145; DB 12; Length 769;
Best Local Similarity 100.0%; Pred. No. 4.9e-70;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 GACACCCCAACCTTTGAGAGAGAGAACTCTAATCAAGAGACTGCTGTTCGAGAAAT 1540
        |||||||
Db 55 GACACCCCAACCTTTGAGAGAGAGAACTCTAATCAAGAGACTGCTGTTCGAGAAAT 114

QY 1541 AAATCTTAAATCTGTGTAATAGAAAACCTGAATATTATTAATAGAAATGCAAT 1600
        |||||||
Db 115 AAATCTTAAATCTGTGTAATAGAAAACCTGAATATTATTAATAGAAATGCAAT 174

QY 1601 CAGGCGCTAGTTTCTTATTAATAAAT 1625
        |||||||
Db 175 CAGGCGCTAGTTTCTTATTAATAAAT 199

RESULT 50
BG960989/c
LOCUS      BG960989
DEFINITION PM2-CT0265-170401-014-d05 CT0265 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BG960989
VERSION     BG960989.1 GI:14374160
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

REFERENCE   1 (bases 1 to 304)
AUTHORS     Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
            Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.P.,
            Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
            Brundstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
            M.J., Soares, F., Brentani, P.P., Peis, L.F., de Souza, S.J. and
            Simpson, A.J.
TITLE       Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
JOURNAL     Proc Natl Acad Sci U S A 97 (7), 4491-4496 (2000)
MEDLINE     20202653
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM2at2-PM2-CT0265-
            170401-014-d05&t3=2001-04-17&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 15
            High quality sequence stop: 286.
FEATURES    source
             Location/Qualifiers
               1..304
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone_11b="CT0265"
               /dev_stage="Adult"
               /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
               SmaI; A mini-library was made by cloning products derived
               from ORESTES PCR (U.S. Letters Patent application No. 196
               716 - Ludwig Institute for Cancer Research) profiles
               into the puc 18 vector. Reverse transcription of tissue
               mRNA and cDNA amplification were performed under low
               stringency conditions."
BASE COUNT  88 a 69 c 55 g 92 t
ORIGIN
Query Match      7.6%; Score 135; DB 13; Length 304;
Best Local Similarity 99.5%; Pred. No. 2.1e-64;
Matches 185; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 928 TGTGGCTATTTTATCTTTTATCTGCTCGAAGGCTACGGAATGCAAGAGCTCAAGACAG 987
        |||||||
Db 245 TGTGGCTATTTTATCTTTTATCTGCTCGAAGGCTACGGAATGCAAGAGCTCAAGACAG 186

QY 988 GAAGCAGAGGCAATTAAGGCAGATGCTAAAAAGCTATTGGAAGCTTCAACTAGGCAC 1047
        |||||||
Db 195 GAAGCAGAGGCAATTAAGGCAGATGCTAAAAAGCTATTGGAAGCTTCAACTAGGCAC 126

QY 1048 ACTGAACACAGCAGACAGAAATTCGCCCTGATGAGATAGTTGTCTGTGCTTGA 1107
        |||||||
Db 125 ACTGATACAGAGAGACAGAAATTCGCCCTGATGAGATAGTTGTCTGTGCTTGA 66

QY 1108 ATTGTA 1113
        |||||||
Db 65 ATTGTA 60

Search completed: October 31, 2002, 11:44:19
Job time : 2040 secs

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GenCore version 5.1.1

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OM nucleic - nucleic search, using sw model

Run on: October 31 2002 08:56:14 : Search time 270 Seconds
(without alignments)
14796.463 Million cell alignments/sec

Title: US-09-854-100-7

Perfect score: 1774

Sequence: 1 agtggaggtacacggggt.....ataggaaagttacgtctatg tttg

Scoring table:

OLIGO_NUC

Gapop 60.0, Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Word size: 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database:

N_Geneseq_101002.*
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2: /SID2/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
3: /SID2/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
4: /SID2/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
5: /SID2/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
6: /SID2/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
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18: /SID2/gcgdata/geneseq/geneseq-emb1/NA2007.DAT.*
19: /SID2/gcgdata/geneseq/geneseq-emb1/NA2008.DAT.*
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22: /SID2/gcgdata/geneseq/geneseq-emb1/NA2011.DAT.*
23: /SID2/gcgdata/geneseq/geneseq-emb1/NA2012.DAT.*
24: /SID2/gcgdata/geneseq/geneseq-emb1/NA2013.DAT.*

Pred. No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	1774	100.0	1774	24	AAI72095 Human GRAIL cDNA
2	1417	79.9	2773	21	AAAI5995 Human protein cles
3	1417	79.9	2796	24	AAI72321 ISIGP 4 cDNA, Hom
4	1080	60.9	1284	21	AAAI5985 Human protein cion
5	824	46.4	2306	22	AAS25884 Human cDNA encoding
6	790	44.5	1135	22	AAI59292 Human polynucleoti
7	722	40.7	1249	24	ABL90796 Human polynucleoti
8	704	39.7	1250	22	AAS26340 Human cDNA encoding
9	497	28.0	2476	22	AAS45511 Human cDNA encoding

ALIGNMENTS

RESULT: 1
AAI72095

10	360	20.3	737	22	AAI61078 Human polynucleoti
11	354	20.0	502	24	ABN19991 Novel ORFX polynuc
12	292	16.5	404	22	AAF66696 Human colon tumour
13	275	15.5	646	24	ABL38246 cDNA encoding colo
14	167	9.4	435	24	ABK45625 Human secreted pro
15	80	4.5	922	22	AAF97896 Human secreted pro
16	78	4.4	810	21	AAC59154 Human ovarian anti
17	78	4.4	1055	24	ABQ42449 Human acrosomal sp
18	77	4.3	912	21	AAZ32934 DNA encoding novel
19	77	4.3	1568	23	ABK43706 Human colon cancer
20	76	4.3	387	22	AAH35391 Human colon cancer
21	76	4.3	613	22	AAH33228 Human colon cancer
22	76	4.3	940	22	ABA77069 Proliferative glom
23	76	4.3	1247	22	AAH35001 Human colon cancer
24	76	4.3	1772	22	ABA06482 Human cDNA SEQ ID
25	76	4.3	2776	24	ABL52661 cDNA encoding nove
26	76	4.3	3789	22	AAS26981 Human immune/haema
27	75	4.2	373	22	AAK59576 Human immune/haema
28	75	4.2	411	22	AAK60386 Human secreted pro
29	75	4.2	558	21	AAC80580 Human secreted pro
30	75	4.2	745	21	AAA87692 Human nervous syst
31	75	4.2	829	23	ABAI2886 Human polynucleoti
32	75	4.2	846	24	ABL90566 Proliferative glom
33	75	4.2	864	22	ABA77055 Human secreted pro
34	75	4.2	882	21	AAC63454 Human secreted pro
35	75	4.2	1243	22	AAS33285 DNA encoding human
36	75	4.2	1355	22	ABA06738 Human cDNA SEQ ID
37	75	4.2	1355	22	AAS29727 Human polynucleoti
38	75	4.2	1355	22	AAI63957 Human cDNA encoding
39	75	4.2	1355	22	AAS31368 cDNA encoding nove
40	75	4.2	1355	22	AAS35029 Human polynucleoti
41	75	4.2	1591	22	ABQ66692 Human tumour necro
42	75	4.2	1605	21	AAA71121 Human Adipose Spec
43	75	4.2	1744	21	AAS7334 cDNA encoding nove
44	75	4.2	1805	21	AAZ48809 Soybean inositol 1
45	75	4.2	2005	22	ABL23356 Human secreted pro
46	75	4.2	2099	22	AAI2681 Human reproductive
47	75	4.2	2099	22	ABL97322 Human testicular a
48	75	4.2	200	22	AAH35162 Human colon cancer
49	74	4.2	247	22	AAH35170 Human colon cancer
50	74	4.2	258	22	AAH67823 Peppermint plant o
51	74	4.2	433	22	AAH35061 Human colon cancer
52	74	4.2	464	21	ABAI3438 Human nervous syst
53	74	4.2	485	22	ABA07627 Human ovarian and
54	74	4.2	485	22	ABA07627 Human reproductive
55	74	4.2	492	21	AAI23322 Human cancer assoc
56	74	4.2	524	20	AAI23322 DNA encoding a hum
57	74	4.2	552	24	ABQ54502 Human ovarian anti
58	74	4.2	559	22	AAH34635 Human colon cancer
59	74	4.2	560	24	ABL92390 Human secreted pro
60	74	4.2	571	21	AAK59622 Human immune/haema
61	74	4.2	604	22	AAI33396 Human secreted pro
62	74	4.2	608	21	AAIB1134 Human secreted pro
63	74	4.2	612	24	ABQ54522 Human ovarian anti
64	74	4.2	640	22	ABA07535 Human ovarian and
65	74	4.2	640	22	AAI00464 Human reproductive
66	74	4.2	640	22	ABK72059 Human cDNA encoding
67	74	4.2	640	24	ABK91651 cDNA encoding nove
68	74	4.2	663	22	AAK60757 Human immune/haema
69	74	4.2	687	20	AAI30321 DNA encoding a hum
70	74	4.2	707	22	AAI198650 Human excretory re
71	74	4.2	707	22	AAI63046 Human kidney relat
72	74	4.2	707	22	AAI63046 Human polynucleoti
73	74	4.2	736	24	ABL90752 Human polynucleoti
74	74	4.2	737	22	AAI199590 Human expressed po
75	74	4.2	737	22	ABA06506 Human cDNA SEQ ID

ID AAI72095 standard; cDNA: 1774 BP.

XX AAI72095;

XX 25-MAR-2002 (first entry)

XX Human GRAIL cDNA.

XX Murine: human; GRAIL; anergy; attenuation; tyrosine phosphorylation; antigenic stimulation; interleukin-2 gene therapy; polymorphism IL-2; KW autoimmune disease; tumour cell cancer; transplant rejection; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
XX CDS 263 1547
XX /*tag= a
XX /product= "GRAIL"

XX WC200195243-A1

XX 15-NOV-2001

XX 11-MAY-2001: 2601W-151545

XX 11-MAY-2000: 2000US-203513P.

XX (STRD) UNIV LELAND STANFORD JUNIOR

XX Ford GS, Bloom D, Fathman GS;

XX WPI: 2002-055597/37

XX P-PSDR: AAR47800.

XX Novel nucleic acid sequences of anergy associated genes, including GRAIL gene useful in the evaluation of pathophysiology of immunotherapy of cancer, autoimmune disease and transplant rejection -

XX Claim 2: Page 45-47: 50pp: English.

XX This sequence encodes human GRAIL protein. The GRAIL gene is an energy associated gene which is upregulated during the early stages of induction of anergy. GRAIL has been shown to attenuate IL-2 transcription in T-cells during response to antigenic stimulation. GRAIL DNA is useful for decreasing the responsiveness of a T cell population, especially synthesis of interleukin-2 (IL-2) in response to antigenic stimulation, by up-regulating GRAIL activity in the T cell population. GRAIL DNA is useful in producing compositions that modulate induction or maintenance of anergy, for gene therapy, mapping functional regions of the encoded protein, to analyse a patient sample for the presence of polymorphisms or alterations in expression of sequences associated with T cell anergy, disease states, genetic predisposition to a disease state, and in studying associated physiological pathways. Modulation of the gene activity in vivo is useful for prophylactic and therapeutic purposes, such as treating autoimmune disease and to enhance immune response to tumour cells, and identification of anergic T cells. GRAIL DNA is useful in the evaluation of the pathophysiology or immunotherapy of cancer, autoimmune disease, and transplant rejection. Genetic sequences involved in anergy induction are useful as markers in the evaluation of specific immunotherapies. Functional characterization of genes involved in anergy induction allows the elucidation of the mechanisms of T cell anergy, including the transcriptional blockade of IL-2, which may be manipulated to regulate T cell responses in human disease. Modulation of expression of GRAIL gene is useful in manipulating the anergic state. The genetic sequences find use alone or in combinations in determining the expression profile of cells relating to anergy, for example in screening of candidate biologically active compounds for modulation of T cell anergy. Expression of GRAIL has been found to block tyrosine phosphorylation of a protein present in T cells during activation.

XX Sequence 1774 BP: 454 A: 432 C: 464 G: 423 T: 1 other;

Query Match	100.0%	Score 1774:	DB 24:	Length 1774:
Best Local Similarity	100.0%	Pred. No. 0:		
Matches 1774:	Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0:
QY 1	AGCTGGAGCTCCACGCGCGGTGGCGCGGTCTAGAACTAGTGTGATCCCGCGCGGTGGCGAGG	60		
DB 1	AGCTGGAGCTCCACGCGCGGTGGCGCGGTCTAGAACTAGTGTGATCCCGCGCGGTGGCGAGG	60		
QY 61	AATTCGGCAAGACGCGCGGTGGCGCGGTCTAGAACTAGTGTGATCCCGCGCGGTGGCGAGG	120		
DB 61	AATTCGGCAAGACGCGCGGTGGCGCGGTCTAGAACTAGTGTGATCCCGCGCGGTGGCGAGG	120		
QY 121	CTCTGGCTGGCACTAGTGTGATCCCGCGGTGGCGCGGTCTAGAACTAGTGTGATCCCGCGGTGGCGAGG	180		
DB 121	CTCTGGCTGGCACTAGTGTGATCCCGCGGTGGCGCGGTCTAGAACTAGTGTGATCCCGCGGTGGCGAGG	180		
QY 181	GGCACTGGCTGGCACTAGTGTGATCCCGCGGTGGCGCGGTCTAGAACTAGTGTGATCCCGCGGTGGCGAGG	240		
DB 181	GGCACTGGCTGGCACTAGTGTGATCCCGCGGTGGCGCGGTCTAGAACTAGTGTGATCCCGCGGTGGCGAGG	240		
QY 241	GGCACTGGCTGGCACTAGTGTGATCCCGCGGTGGCGCGGTCTAGAACTAGTGTGATCCCGCGGTGGCGAGG	300		
DB 241	GGCACTGGCTGGCACTAGTGTGATCCCGCGGTGGCGCGGTCTAGAACTAGTGTGATCCCGCGGTGGCGAGG	300		
QY 301	TGGCTGGCTGGCACTAGTGTGATCCCGCGGTGGCGCGGTCTAGAACTAGTGTGATCCCGCGGTGGCGAGG	360		
DB 301	TGGCTGGCTGGCACTAGTGTGATCCCGCGGTGGCGCGGTCTAGAACTAGTGTGATCCCGCGGTGGCGAGG	360		
QY 361	ACCGCTGGCTGGCACTAGTGTGATCCCGCGGTGGCGCGGTCTAGAACTAGTGTGATCCCGCGGTGGCGAGG	420		
DB 361	ACCGCTGGCTGGCACTAGTGTGATCCCGCGGTGGCGCGGTCTAGAACTAGTGTGATCCCGCGGTGGCGAGG	420		
QY 421	TGGCTGGCTGGCACTAGTGTGATCCCGCGGTGGCGCGGTCTAGAACTAGTGTGATCCCGCGGTGGCGAGG	480		
DB 421	TGGCTGGCTGGCACTAGTGTGATCCCGCGGTGGCGCGGTCTAGAACTAGTGTGATCCCGCGGTGGCGAGG	480		
QY 481	GGCACTGGCTGGCACTAGTGTGATCCCGCGGTGGCGCGGTCTAGAACTAGTGTGATCCCGCGGTGGCGAGG	540		
DB 481	GGCACTGGCTGGCACTAGTGTGATCCCGCGGTGGCGCGGTCTAGAACTAGTGTGATCCCGCGGTGGCGAGG	540		
QY 541	TGGCTGGCTGGCACTAGTGTGATCCCGCGGTGGCGCGGTCTAGAACTAGTGTGATCCCGCGGTGGCGAGG	600		
DB 541	TGGCTGGCTGGCACTAGTGTGATCCCGCGGTGGCGCGGTCTAGAACTAGTGTGATCCCGCGGTGGCGAGG	600		
QY 601	AGTCTGGCTGGCACTAGTGTGATCCCGCGGTGGCGCGGTCTAGAACTAGTGTGATCCCGCGGTGGCGAGG	660		
DB 601	AGTCTGGCTGGCACTAGTGTGATCCCGCGGTGGCGCGGTCTAGAACTAGTGTGATCCCGCGGTGGCGAGG	660		
QY 661	TGGCTGGCTGGCACTAGTGTGATCCCGCGGTGGCGCGGTCTAGAACTAGTGTGATCCCGCGGTGGCGAGG	720		
DB 661	TGGCTGGCTGGCACTAGTGTGATCCCGCGGTGGCGCGGTCTAGAACTAGTGTGATCCCGCGGTGGCGAGG	720		
QY 721	TGGCTGGCTGGCACTAGTGTGATCCCGCGGTGGCGCGGTCTAGAACTAGTGTGATCCCGCGGTGGCGAGG	780		
DB 721	TGGCTGGCTGGCACTAGTGTGATCCCGCGGTGGCGCGGTCTAGAACTAGTGTGATCCCGCGGTGGCGAGG	780		
QY 781	TGGCTGGCTGGCACTAGTGTGATCCCGCGGTGGCGCGGTCTAGAACTAGTGTGATCCCGCGGTGGCGAGG	840		
DB 781	TGGCTGGCTGGCACTAGTGTGATCCCGCGGTGGCGCGGTCTAGAACTAGTGTGATCCCGCGGTGGCGAGG	840		
QY 841	AGTCTGGCTGGCACTAGTGTGATCCCGCGGTGGCGCGGTCTAGAACTAGTGTGATCCCGCGGTGGCGAGG	900		
DB 841	AGTCTGGCTGGCACTAGTGTGATCCCGCGGTGGCGCGGTCTAGAACTAGTGTGATCCCGCGGTGGCGAGG	900		
QY 901	TGGCTGGCTGGCACTAGTGTGATCCCGCGGTGGCGCGGTCTAGAACTAGTGTGATCCCGCGGTGGCGAGG	960		
DB 901	TGGCTGGCTGGCACTAGTGTGATCCCGCGGTGGCGCGGTCTAGAACTAGTGTGATCCCGCGGTGGCGAGG	960		
QY 961	TGGCTGGCTGGCACTAGTGTGATCCCGCGGTGGCGCGGTCTAGAACTAGTGTGATCCCGCGGTGGCGAGG	1020		
DB 961	TGGCTGGCTGGCACTAGTGTGATCCCGCGGTGGCGCGGTCTAGAACTAGTGTGATCCCGCGGTGGCGAGG	1020		

74 CCGAGAGCTGCATCTGGGGACACTGTGTGCTTACGCTAGCTGCTCTGGCTCCGACG 133

[illegible]

Db 912 CAATCTGTGTCAGTGTATTCCTCATCTTCAGAACCCAACTTTGAAGAAGAGC 971
 Qy 1506 AAATCTCTAATCAAGAGAGCTGCTTGGAGAAATTAATCTTAAATCTGTCTAAATAGA 1565
 Db 972 AAATCTCTAATCAAGAGAGCTGCTTGGAGAAATTAATCTTAAATCTGTCTAAATAGA 1031
 Qy 1566 AAATCTCTAATCAAGAGAGCTGCTTGGAGAAATTAATCTTAAATCTGTCTAAATAGA 1625
 Db 1032 AAATCTCTAATCAAGAGAGCTGCTTGGAGAAATTAATCTTAAATCTGTCTAAATAGA 1091
 Qy 1626 TGGATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1685
 Db 1092 TGGATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1151
 Qy 1686 ATAGTTAAA 1694
 Db 1152 ATAGTTAAA 1160
 RESULT 6
 ID AAI59292 standard: cDNA; 1135 BP.
 AC AAI59292;
 DT 22-OCT-2001 (first entry)
 DE Human polynucleotide SEQ ID NO 1495.
 KW Human; neurotrophic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200153312-A1.
 PD 26-JUL-2001.
 XX 26-DEC-2000; 2000WO-0534263.
 XX 21-JAN-2000; 2000US-0488725.
 XX 25-APR-2000; 2000US-055317.
 XX 08-JUL-2000; 2000US-0598042.
 XX 19-JUL-2000; 2000US-0620312.
 XX 03-AUG-2000; 2000US-0653450.
 XX 14-SEP-2000; 2000US-0662191.
 XX 19-OCT-2000; 2000US-0693036.
 XX 25-NOV-2000; 2000US-0727344.
 PA (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 XX WPI: 2001-442253/47.
 DR P-PSDB: AAM40136.
 XX Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 PS Claim 1; SEQ ID NO 1495; 10078pp; English.
 XX The invention relates to human nucleic acids (AAI57798-AAI61369) and
 CC the encoded polypeptides (AAM38642-AAM42213) with neurotropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous

CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 XX

SQ Sequence 1135 BP; 367 A; 218 C; 234 G; 316 T; 0 other;

Query Match 44 5%; Score 790; DB 22; Length 1135;

Best Local Similarity 99.7%; Pred. No. 1;

Matches 940; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 752 GTAGACATTTGTCATCATGATCGGCAATCTGAAGAGCACAAAAATTCGCAATCTATT 811

Db 71 GTAGACATTTGTCATCATGATCGGCAATCTGAAGAGCACAAAAATTCGCAATCTATT 130

Qy 812 CAAAGAGGCATACAAAGTGACATGTCATAGAGTAGGAAAAAACAATGGCCCTTGGGTG 871

Db 131 CAAAGAGGCATACAAAGTGACATGTCATAGAGTAGGAAAAAACAATGGCCCTTGGGTG 190

Qy 872 AATCACTATTCAATTTTTTTCGTCCTCTTTTATTATTACGGCGCAACTGTG 931

Db 191 AATCACTATTCAATTTTTTTCGTCCTCTTTTATTATTACGGCGCAACTGTG 250

Qy 932 GGTATTTTATCTTTTATTTCTCTCTGAGGCTACGAGCTCAAGCAGGAAG 991

Db 251 GGTATTTTATCTTTTATTTCTCTGAGGCTACGAGCTCAAGCAGGAAG 310

Qy 992 CACAGGCAATTAAGGCAGATGCTAAAAAGCTATTGAAGGCTTCAACTAGGCACACTG 1051

Db 311 CACAGGCAATTAAGGCAGATGCTAAAAAGCTATTGAAGGCTTCAACTAGGCACACTG 370

Qy 1052 AAACAAGGAGACAAGGAAATTCGCTGATGAGATAGTGTGCTGTGCAATTGAATTG 1111

Db 371 AAACAAGGAGACAAGGAAATTCGCTGATGAGATAGTGTGCTGTGCAATTGAATTG 430

Qy 1112 TATAAACCAATGATTTGGTAGCATCTTAACGTGCACCATATTTTCCATTAAGACATGT 1171

Db 431 TATAAACCAATGATTTGGTAGCATCTTAACGTGCACCATATTTTCCATTAAGACATGT 490

Qy 1172 GTTACCCATGCTGTAAACACAAAGACTTGCCTCATGTGCAATGTGACATCTCAAA 1231

Db 491 GTTACCCATGCTGTAAACACAAAGACTTGCCTCATGTGCAATGTGACATCTCAAA 550

Qy 1232 GCTTTGGGAATTCAGGCTGATTTGAAGATGATGATGATGATGATGATGATGATGAT 1291

Db 551 GCTTTGGGAATTCAGGCTGATTTGAAGATGATGATGATGATGATGATGATGATGAT 610

Qy 1292 AATGAATATCTAATAGTGCCTCTCCCATGAAGAGGATAATCGCAGGAGACCGCATCA 1351

Db 611 AATGAATATCTAATAGTGCCTCTCCCATGAAGAGGATAATCGCAGGAGACCGCATCA 670

Qy 1352 TCTGGATATGCTTTCAGTACAGGAAACAGATGAACCGCTCTGGAGGAACACGTGCAATCA 1411

Db 671 TCTGGATATGCTTTCAGTACAGGAAACAGATGAACCGCTCTGGAGGAACACGTGCAATCA 730

Qy 1412 ACAATGAAGCTACAGCTGTAAACCATGAAGCAAAATTTCTGTCAGTGGATGTTATT 1471

Db 731 ACAATGAAGCTACAGCTGTAAACCATGAAGCAAAATTTCTGTCAGTGGATGTTATT 790

Qy 1472 CTTATGTTNSACAAACCCCAACCTTTTGAAGAAGACGAAACTCTTAATCAAGAGACTGCTGTT 1531

Db 791 CTTATGTTNSACAAACCCCAACCTTTTGAAGAAGACGAAACTCTTAATCAAGAGACTGCTGTT 850

Qy 1532 CGAGAAATTAATCTTAAATCTGTGTAATAGAAAACTTGAAACCATTAATTAATACAGA 1591

Db 851 CGAGAAATTAATCTTAAATCTGTGTAATAGAAAACTTGAAACCATTAATTAATACAGA 910

QY 1592 ACTGCCAATCAGGCGCTAGTCTTATTATAAATTCGATAAATTTAATAAATAAGACTG 1651
 Db 911 ACTGCCAATCAGGCGCTAGTCTTATTATAAATTCGATAAATTTAATAAATAAGACTG 970
 QY 1652 ATACTGAATGCTCAGATGACTAATATTATGCTATAGTTAA 1694
 Db 971 ATACTGAATGCTCAGATGACTAATATTATGCTATAGTTAA 1013

RESULT 7
 ABL90796
 ID ABL90796 standard; cDNA; 1249 bp.
 XX
 AC ABL90796;
 XX
 DT 24-MAY-2002 (first entry)
 XX
 DE Human polynucleotide SEQ ID NO 1358.
 XX
 FW cytosolic; immunosuppressive; neotropic; neuroprotective; antiviral;
 KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;
 KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW candiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein; gene; ss
 XX
 OS Homo sapiens.
 XX
 PN WO200190304-A2.
 XX
 PD 29-NOV-2001.
 XX
 PF 18-MAY-2001; 2001WO-US16450
 XX
 PR 19-MAY-2000; 2000US-205515P.
 XX
 PA (HUMA-) HUMAN GENOME SRT IN
 XX
 PI Birse CE, Rosen CA;
 DR WPI: 2002-1225-A,16.
 DR P-PSDB: ABB90387.
 XX
 PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
 PT prevention of neural, immune system, muscular, reproductive,
 PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
 PT disorders
 XX
 PS Claim 4; SEQ ID NO 1358. 2001pp - Sequence listing: English.
 XX
 CC The invention relates to novel genes (AB90442-AB90453) and proteins
 CC (AB90440-AB90444) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
 CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
 CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;
 CC (d) wound healing; (e) neurological diseases e.g. Alzheimer's disease and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note. The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
 XX
 SQ Sequence 1249 bp; 379 A; 258 C; 273 G; 335 T; 4 other;

Query Match 40.7%; Score 722; DB 24; Length 1249;
 Best Local Similarity 99.4%; Pred No

Matches	1142;	Conservative	0;	Mismatches	6;	Indels	1;	Gaps	1;
QY	547	CTGTACCCGCGCACGAAATTTTCACGGTGCCTCCAGGGTTTGGGGAACACCGTGCAGACTCTC	606						
Db	18	CTGTAAACCCGCGCACGAAATTTTCACGGTGCCTCCAGGGTTTGGGGAACACCGTGCAGACTCTC	77						
QY	607	TTGGTTGGGCTCTATCAACGCGGCGGCGGCTCTACCTTCGTCAGACAAGATTCATCTGGC	666						
Db	78	TTGGTTGGGCTCTATCAACGCGGCGGCGGCTCTACCTTCGTCAGACAAGATTCATCTGGC	137						
QY	667	TTATGAGAGATGGGCGCTCTGGAGCGCTCATCTTAACTTCCCGGAGCCCGCAATGAGGT	726						
Db	138	TTATGAGAGAGGCGGCGCTCTGGAGCGCTCATCTTAACTTCCCGGAGCCCGCAATGAGGT	197						
QY	727	CATCCCGCATGTCTCACCCGGGTGCAGTAGACACATTTGTTGCAATCATGTGCGCAATCTGAA	786						
Db	198	CATCCCGCATGTCTCACCCGGGTGCAGTAGACATTTTGAATCATGTGCGCAATCTGAA	257						
QY	787	AGGCACAAAAATTTCTGCAATCTATTCAAAGAGCATACAAAGTGACAATGGTGCATAGAAGT	846						
Db	258	AGGCACAAAAATTTCTGCAATCTATTCAAAGAGCATACAAAGTGACAATGGTGCATAGAAGT	317						
QY	847	AGGGAACAAACATGGCCCTTGGGTGAATCACTATTCAATTTTTTTCGTTTCTGTGCTCT	906						
Db	318	AGGGAACAAACATGGCCCTTGGGTGAATCACTATTCAATTTTTTTCGTTTCTGTGCTCT	377						
QY	907	TTTTTATTATACGGCGCAACTGTGGGCTATTTTATCTTTTATCTGCTCGAAGGCTACG	966						
Db	378	TTTTTATTATACGGCGCAACTGTGGGCTATTTTATCTTTTATCTGCTCGAAGGCTACG	437						
QY	967	GAATGCAAGAGCTCAAAGCAGGAGCAGGCAATTTAAAGGCGAGATGCTAAAAAGCTAT	1026						
Db	438	GAATGCAAGAGCTCAAAGCAGGAGCAGGCAATTTAAAGGCGAGATGCTAAAAAGCTAT	497						
QY	1027	TGGAGAGCTTCACTAGGCACACTGAAACAGAGAGCAGAGG-AAATTGGCCCTGTATGAG	1085						
Db	498	TGGAGAGCTTCACTAGGCACACTGAAACAGAGAGCAGAGG-AAATTGGCCCTGTATGAG	557						
QY	1086	ATAGTTGTGCTGTGTGCTGATTTGATTTATATAAATCAATTTGATGCTGCTTAAAGCT	1145						
Db	558	ATAGTTGTGCTGTGTGCTGATTTGATTTATATAAATCAATTTGATGCTGCTTAAAGCT	617						
QY	1146	GCACCATATTTTCCATATAGACATGTGTTGACCCATGCGCTGTTAAACACAGAGCTTCC	1205						
Db	618	GCACCATATTTTCCATATAGACATGTGTTGACCCATGCGCTGTTAAACACAGAGCTTCC	677						
QY	1206	CCAGTGCCTAAATGTGACATACCTCAAGCTTTGGGAATTCAGGTGATGTTGAAGATGGAT	1265						
Db	678	CCAGTGCCTAAATGTGACATACCTCAAGCTTTGGGAATTCAGGTGATGTTGAAGATGGAT	737						
QY	1266	CAGTGTCTTTTACAGCTGCTTCTATCTTAAATATCTATATGCTGCTGCTGCTGCTGCTGCT	1325						
Db	738	CAGTGTCTTTTACAGCTGCTTCTATCTTAAATATCTATATGCTGCTGCTGCTGCTGCTGCT	797						
QY	1326	AGCATATGCTGACGAGACCGCATCATCTGGATATGCTTCACTACAGGAGACAGATGAC	1385						
Db	798	AGCATATGCTGACGAGACCGCATCATCTGGATATGCTTCACTACAGGAGACAGATGAC	857						
QY	1386	CCATTTCTGAGAGAAATACATGCTGCTTAAATGCTTAAAGCTTAAAGCTTAAAGCTTAA	1445						
Db	858	CCATTTCTGAGAGAAATACATGCTGCTTAAATGCTTAAAGCTTAAAGCTTAAAGCTTAA	917						
QY	1446	CAATTTCTGAGAGAAATACATGCTGCTTAAATGCTTAAAGCTTAAAGCTTAAAGCTTAA	1505						
Db	918	CAATTTCTGAGAGAAATACATGCTTAAATGCTTAAAGCTTAAAGCTTAAAGCTTAAAG	977						
QY	1506	AAATCTCTTAAATGAGAGAAATGCTGCTGCTTAAATGCTTAAAGCTTAAAGCTTAAAG	1565						
Db	978	AAATCTCTTAAATGAGAGAAATGCTGCTGCTTAAATGCTTAAAGCTTAAAGCTTAAAG	1037						
QY	1566	AAATCTGAGAGAAATGAGAGAAATGAGAGAAATGAGAGAAATGAGAGAAATGAGAGAA	1625						
Db	1038	AAATCTGAGAGAAATGAGAGAAATGAGAGAAATGAGAGAAATGAGAGAAATGAGAGAA	1097						

OY 1626 TGGATAAATTAATAAATAAGAGTGATCTGAAGAGTGTCTGAGATGACTAATATTATGCT 1685
Db 1098 TGGATAAATTAATAAATAAGAGTGATCTGAAGAGTGTCTGAGATGACTAATATTATGCT 1157
OY 1686 ATAGTTAAA 1694
Db 1158 ATAGTTAAA 1166

RESULT 8
ID AAS26340 standard: cDNA; 1250 BP
AC AAS26340:
XX 07-NOV-2001 (first entry)
XX Human cDNA encoding a novel secreted protein, Seq ID 519.
DE Human: immunosuppressive; antiarthritic; ss; antirheumatic;
KW cytotatic; cardiac; vasotropic; cerebroprotective; neutropic;
KW neuroprotective; antibacterial; virucide; fungicide; ophthalmological;
KW vulnary; secreted protein; rheumatoid arthritis;
KW hyperproliferative disorder; cardiovascular disorder; cardiac arrest;
KW cerebrovascular disorder; cerebral ischaemia; angiogenesis;
KW nervous system disorder; Alzheimer's disease; infection; ocular disorder;
KW corneal infection; wound healing; epithelial cell proliferation;
KW skin ageing; food additive; preservative; antiproliferative.
XX Homo sapiens.
XX W0200155322-A2
PN 02-AUG-2001.
PD 02-AUG-2001.
XX 17-JAN-2001; 2001ko-HS01341
XX 31-JAN-2000; 2000ns-0170n65
PR 04-FEB-2000; 2000ns-0180n29
PR 24-FEB-2000; 2000ns-0184n64
PR 02-MAR-2000; 2000ns-0185n60
PR 16-MAR-2000; 2000ns-0189n74
PR 17-MAR-2000; 2000ns-0190n76
PR 18-APR-2000; 2000ns-0198123
PR 19-MAY-2000; 2000ns-0205515
PR 02-JUN-2000; 2000ns-0209467
PR 28-JUN-2000; 2000ns-0214n86
PR 30-JUN-2000; 2000ns-0215135
PR 07-JUL-2000; 2000ns-0216547
PR 09-JUL-2000; 2000ns-0216n80
PR 11-JUL-2000; 2000ns-0217n87
PR 14-JUL-2000; 2000ns-0217n96
PR 14-JUL-2000; 2000ns-0218n93
PR 26-JUL-2000; 2000ns-0220n93
PR 26-JUL-2000; 2000ns-0220n94
PR 14-AUG-2000; 2000ns-0224518
PR 14-AUG-2000; 2000ns-0224519
PR 14-AUG-2000; 2000ns-0225213
PR 14-AUG-2000; 2000ns-0225214
PR 14-AUG-2000; 2000ns-0225266
PR 14-AUG-2000; 2000ns-0225267
PR 14-AUG-2000; 2000ns-0225268
PR 14-AUG-2000; 2000ns-0225270
PR 14-AUG-2000; 2000ns-0225277
PR 14-AUG-2000; 2000ns-0225757
PR 14-AUG-2000; 2000ns-0225n58
PR 14-AUG-2000; 2000ns-0227n59
PR 18-AUG-2000; 2000ns-0228279
PR 22-AUG-2000; 2000ns-0228681
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PR 24-AUG-2000; 2000ns-0227000
PR 30-AUG-2000; 2000ns-0228924
PR 01-SEP-2000; 2000ns-0229287
PR 01-SEP-2000; 2000ns-0229343
PR 01-SEP-2000; 2000ns-0229344
PR 01-SEP-2000; 2000ns-0229345
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PR 05-SEP-2000; 2000ns-0229513
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PR 08-SEP-2000; 2000ns-0232081
PR 12-SEP-2000; 2000ns-0231968
PR 14-SEP-2000; 2000ns-0232397
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PR 14-SEP-2000; 2000ns-0232399
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PR 14-SEP-2000; 2000ns-0233065
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PR 21-SEP-2000; 2000ns-0234274
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PR 26-SEP-2000; 2000ns-0235484
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PR 02-OCT-2000; 2000ns-0237038
PR 02-OCT-2000; 2000ns-0237039
PR 02-OCT-2000; 2000ns-0237040
PR 13-OCT-2000; 2000ns-0239935
PR 13-OCT-2000; 2000ns-0239937
PR 20-OCT-2000; 2000ns-0240960
PR 20-OCT-2000; 2000ns-0241221
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PR 20-OCT-2000; 2000ns-0241786
PR 20-OCT-2000; 2000ns-0241787
PR 20-OCT-2000; 2000ns-0241808
PR 20-OCT-2000; 2000ns-0241809
PR 20-OCT-2000; 2000ns-0241826
PR 01-NOV-2000; 2000ns-0244617
PR 08-NOV-2000; 2000ns-0246474
PR 08-NOV-2000; 2000ns-0246475
PR 08-NOV-2000; 2000ns-0246476
PR 08-NOV-2000; 2000ns-0246477
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PR 08-NOV-2000; 2000ns-0246524
PR 08-NOV-2000; 2000ns-0246525
PR 08-NOV-2000; 2000ns-0246526
PR 08-NOV-2000; 2000ns-0246527
PR 08-NOV-2000; 2000ns-0246528
PR 08-NOV-2000; 2000ns-0246532
PR 08-NOV-2000; 2000ns-0246603
PR 08-NOV-2000; 2000ns-0246610
PR 08-NOV-2000; 2000ns-0246611
PR 08-NOV-2000; 2000ns-0246613
PR 17-NOV-2000; 2000ns-0249207
PR 17-NOV-2000; 2000ns-0249208
PR 17-NOV-2000; 2000ns-0249209
PR 17-NOV-2000; 2000ns-0249210

CC vivo and in vitro. It exhibits immunocontraceptive properties when
 CC used to actively immunise male hamsters. Similarly, p34 has potential
 CC for use in an immunocontraceptive vaccine in humans. p34
 CC is specifically expressed in the epididymis, which supports its
 CC potential as an immunocontraceptive target. An immunocontraceptive
 CC vaccine may comprise antigenic fragments of p34 (AA52292, AA52293),
 CC and an immune response should be generated against the p34 fragments
 CC when administered to men. As the blood-testis barrier is not present in
 CC the epididymis, the antibodies should reach the spermatozoa and
 CC neutralise the fertilising ability of the spermatozoa, thus conferring
 CC an immunocontraceptive protection.

XX Sequence 912 BP: 187 A: 279 C: 286 G: 160 T: 0 other:

SQ Query Match 4.3% Score 77; DB 21; Length 912;

Best Local Similarity 100.0% #Pred. No 1 9e-28;

Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGCGGTGGCGGCGCTCTAGAACTAGTGGATCCCGGCGCTGAGC 60

Db 7 AGCTGGAGCTCCACCGCGGTGGCGGCGCTCTAGAACTAGTGGATCCCGGCGCTGAGC 66

QY 61 AATTGGCAGCAGGCGGA 77

Db 67 AATTGGCAGCAGGCGGA 83

RESULT 19

ABK43706

ID ABK43706 standard; cDNA; 1568 BP

AC ABK43706;

XX

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XX

CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
CC present invention.
CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
CC missing at time of publication, meaning no sequences are present for
CC SEQ ID NO:1027 to 1052, 7921 and 7922.
XX
XX
SQ Sequence 387 BP; 79 A, 129 C, 104 G, 70 T, 5 other;
Query Match 4.3%; Score 76; DB 22; Length 387;
Best Local Similarity 100.0%; Pred. No. 6.2e-28;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCTGGAGCTCCACCGCGGTGGCGGCGCTCTAGAACTACTGATCTAGATCCGCGGCTGCGAGG 60
DQ 35 AGCTGGAGCTCCACCGCGGTGGCGGCGCTCTAGAACTACTGATCTAGATCCGCGGCTGCGAGG 79
QY 61 AATTCGGCAGCAGCGG 76
DQ 95 AATTCGGCAGCAGCGG 110
RESULT 21
ID AAH33228 standard; cDNA; 613 BP.
XX
XX
AC AAH33228;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen encoding cDNA SEQ ID NO:284.
XX
DE Human: colon cancer; colon cancer antigen; diagnosis; detection;
KW colorectal carcinoma; ss.
XX
XX Homo sapiens.
XX
XX WO200122920-A2
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-0526524.
XX
PF 29-SEP-1999; 90US-0157137.
XX
PR 03-NOV-1999; 99US-0163280.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
XX WPI: 2001-235357/24.
XX
XX P-PSDB: AAG73797.
XX
XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
XX useful for preventing, diagnosing and/or treating colorectal cancers -
XX
XX Claim 1; Page 2411; 9803pp; English.
XX
XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
XX cancer-associated nucleic acid molecules (N) and proteins (P), where
XX the proteins are collectively known as colon cancer antigens. The colon
XX cancer antigens have cytostatic activity and can be used in gene
XX therapy and vaccine production. N and P may be used in the prevention,
XX diagnosis and treatment of diseases associated with inappropriate P
XX expression. For example, N and P may be used to treat disorders
XX associated with decreased expression by rectifying mutations or deletions
XX in a patient's genome that affect the activity of P by expressing
XX inactive proteins or to supplement the patient's own production of P.
XX Additionally, N may be used to produce the colon cancer-associated Ps,
XX by inserting the nucleic acids into a host cell and culturing the cell.
XX to express the proteins N and P can be used in the prevention, diagnosis
XX and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
XX and AAB77789 represent sequences used in the exemplification of the

CC present invention.
CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
CC missing at time of publication, meaning no sequences are present for
CC SEQ ID NO:1027 to 1052, 7921 and 7922.
XX
XX
SQ Sequence 613 BP; 165 A, 179 C, 151 G, 111 T, 7 other;
Query Match 4.3%; Score 76; DB 22; Length 613;
Best Local Similarity 100.0%; Pred. No. 6.3e-28;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCTGGAGCTCCACCGCGGTGGCGGCGCTCTAGAACTACTGATCTAGATCCGCGGCTGCGAGG 60
DQ 20 AGCTGGAGCTCCACCGCGGTGGCGGCGCTCTAGAACTACTGATCTAGATCCGCGGCTGCGAGG 79
QY 61 AATTCGGCAGCAGCGG 76
DQ 80 AATTCGGCAGCAGCGG 95
RESULT 22
ID ABA77069 standard; DNA; 940 BP.
XX
XX
AC ABA77069;
XX
DT 24-JAN-2002 (first entry)
XX
DE Proliferative glomerular nephritis-associated gene sequence SEQ ID-76
XX
XX kat; proliferative glomerular nephritis-associated gene; TRDH;
KW stromal cell derived factor-2; prostacyclin-stimulation factor;
KW TSC-22 like protein 2; kidney disease; diagnosis; kidney disorder;
KW proliferative glomerular nephritis; ds.
XX
XX Rattus norvegicus.
XX
XX WO200173022-A1.
XX
XX 04-OCT-2001.
XX
XX 23-MAR-2001; 2001WO-3F03623.
XX
XX 29-MAR-2000; 2000JP-0090137.
XX
XX (KYOW) KYOWA HAKKO KOGYO KK.
XX
XX Takeuchi K, Sekine S, Kikuchi Y, Sakurada K;
XX
XX WPI: 2001-616500/71.
XX
XX New DNA having increased expression in kidney tissues affected by
XX proliferative glomerular nephritis for diagnosis and treatment of
XX kidney disease and promotion of repair of damaged kidney tissue -
XX
XX Claim 16; Page 210-211; 314pp; Japanese.
XX
XX The present invention describes polynucleotide sequences of rat origin
XX which encode proteins having increased expression in kidney tissues
XX affected by proliferative glomerular nephritis. The proliferative
XX glomerular nephritis-associated polynucleotide and protein sequence have
XX nephrotropic activity. The polynucleotides can be used in the diagnosis,
XX treatment and prevention of kidney disease, especially of proliferative
XX glomerular nephritis, and in the repair of tissues damaged by kidney
XX disease. ABA77002 to ABA77154 and AAG68138 to AAG68147 represent
XX sequences given in the exemplification of the present invention.
XX
XX Sequence 948 BP; 257 A; 221 C; 266 G; 164 T; 32 other;
Query Match 4.3%; Score 76; DB 22; Length 940;
Best Local Similarity 100.0%; Pred. No. 6.3e-28;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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PP 05-SEP-2000; 2000US-0229513
PP 06-SEP-2000; 2000US-0230437
PP 06-SEP-2000; 2000US-0230438
PP 08-SEP-2000; 2000US-0231242
PP 08-SEP-2000; 2000US-0231243
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PP 08-SEP-2000; 2000US-0231244
PP 08-SEP-2000; 2000US-0231413
PP 08-SEP-2000; 2000US-0231414
PP 08-SEP-2000; 2000US-0232080
PP 12-SEP-2000; 2000US-0232081
PP 14-SEP-2000; 2000US-0231968
PP 14-SEP-2000; 2000US-0232392
PP 14-SEP-2000; 2000US-0232398
PP 14-SEP-2000; 2000US-0232399
PP 14-SEP-2000; 2000US-0232400
PP 14-SEP-2000; 2000US-0232401
PP 14-SEP-2000; 2000US-0233063
PP 14-SEP-2000; 2000US-0233064
PP 14-SEP-2000; 2000US-0233065
PP 21-SEP-2000; 2000US-0233065
PP 21-SEP-2000; 2000US-0233233
PP 21-SEP-2000; 2000US-0234274
PP 25-SEP-2000; 2000US-0234497
PP 25-SEP-2000; 2000US-0234998
PP 26-SEP-2000; 2000US-0235484
PP 27-SEP-2000; 2000US-0235834
PP 27-SEP-2000; 2000US-0235836
PP 29-SEP-2000; 2000US-0236327
PP 29-SEP-2000; 2000US-0236367
PP 29-SEP-2000; 2000US-0236368
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PP 29-SEP-2000; 2000US-0236370
PP 02-OCT-2000; 2000US-0236802
PP 02-OCT-2000; 2000US-0237037
PP 02-OCT-2000; 2000US-0237038
PP 02-OCT-2000; 2000US-0237039
PP 02-OCT-2000; 2000US-0237040
PP 13-OCT-2000; 2000US-0239935
PP 13-OCT-2000; 2000US-0239937
PP 20-OCT-2000; 2000US-0240960
PP 20-OCT-2000; 2000US-0241231
PP 20-OCT-2000; 2000US-0241785
PP 20-OCT-2000; 2000US-0241786
PP 20-OCT-2000; 2000US-0241787
PP 20-OCT-2000; 2000US-0241808
PP 20-OCT-2000; 2000US-0241809
PP 20-OCT-2000; 2000US-0241826
PP 01-NOV-2000; 2000US-0244617
PP 08-NOV-2000; 2000US-0246474
PP 08-NOV-2000; 2000US-0246475
PP 08-NOV-2000; 2000US-0246476
PP 08-NOV-2000; 2000US-0246477
PP 08-NOV-2000; 2000US-0246478
PP 08-NOV-2000; 2000US-0246523
PP 08-NOV-2000; 2000US-0246524
PP 08-NOV-2000; 2000US-0246525
PP 08-NOV-2000; 2000US-0246526
PP 08-NOV-2000; 2000US-0246527
PP 08-NOV-2000; 2000US-0246528
PP 08-NOV-2000; 2000US-0246532
PP 08-NOV-2000; 2000US-0246532
PP 08-NOV-2000; 2000US-0246609
PP 08-NOV-2000; 2000US-0246610
PP 08-NOV-2000; 2000US-0246611
PP 08-NOV-2000; 2000US-0246613
PP 17-NOV-2000; 2000US-0249207
PP 17-NOV-2000; 2000US-0249208
PP 17-NOV-2000; 2000US-0249209
PP 17-NOV-2000; 2000US-0249210
PP 17-NOV-2000; 2000US-0249211
PP 17-NOV-2000; 2000US-0249212
PP 17-NOV-2000; 2000US-0249213
PP 17-NOV-2000; 2000US-0249214
PP 17-NOV-2000; 2000US-0249215
PP 17-NOV-2000; 2000US-0249216

FR 17-NOV-2000; 2000US-0249217
FR 17-NOV-2000; 2000US-0249218
FR 17-NOV-2000; 2000US-0249244
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FR 17-NOV-2000; 2000US-0249245
FR 17-NOV-2000; 2000US-0249245
FR 17-NOV-2000; 2000US-0249265
FR 17-NOV-2000; 2000US-0249297
FR 17-NOV-2000; 2000US-0249299
FR 17-NOV-2000; 2000US-0249300
FR 01-DEC-2000; 2000US-0250160
FR 01-DEC-2000; 2000US-0250391
FR 05-DEC-2000; 2000US-0251030
FR 05-DEC-2000; 2000US-0251988
FR 05-DEC-2000; 2000US-0256719
FR 06-DEC-2000; 2000US-0251479
FR 08-DEC-2000; 2000US-0251856
FR 08-DEC-2000; 2000US-0251868
FR 08-DEC-2000; 2000US-0251869
FR 08-DEC-2000; 2000US-0251989
FR 08-DEC-2000; 2000US-0251990
FR 11-DEC-2000; 2000US-0254097
FR 05-JAN-2001; 2001US-0259678
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX
DR WPI; 2001-465460/50.
XX
XX P-PSDB; AAU17064.
XX
PT Novel polypeptides useful for diagnosing, treating, preventing and/or
PT prognosing disorders related to the proteins, including cancers, immune
PT disorders and neuronal disorders
XX
PS Claim 1: SEQ ID No 16; 880pp; English.
XX
XX The invention relates to novel isolated polypeptides (I), and
XX polynucleotides (II). (I), (II) and the antibody to (I) are useful for
XX diagnosing, preventing and treating diseases including immune system
XX disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
XX disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
XX transplant rejections and graft versus host disease, infectious diseases
XX (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and
XX other blood-related disorders (sickle cell anaemia), myeloproliferative
XX disorders, primary haematopoietic disorders, hyperproliferative
XX disorders (e.g. Gaucher's disease and cancer), neurodegenerative
XX disorders (e.g. Alzheimer's disease, Parkinson's disease), chromosomal
XX abnormalities (Down syndrome), ischaemic injury (e.g. stroke), renal
XX disorders (e.g. glomerulonephritis), cardiovascular disorders
XX (e.g. arrhythmia), respiratory disorders, dermatological disorders, in
XX wound healing, epithelial cell proliferation, endocrine disorders (e.g.
XX Addison's disease), reproductive system disorders, gastrointestinal
XX disorder (inflammatory disorders), liver disorders (cirrhosis),
XX as stimulators of B-cell responsiveness to pathogens, activators of
XX T-cells, to induce higher affinity antibodies, and as a means to induce
XX tumour proliferation in pathologies e.g. acquired immune deficiency
XX syndrome (AIDS). AAS26976-AAS27850 represent novel signal transduction
XX pathway protein coding sequences and PCR primers of the invention.
XX

Query Match 4.3%, Score 76, DB 22, Length 3789;
Best Local Similarity 100.0%, Pred. NO. 6.3e-28,
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGCGGCGGCGGCGGCTCTAGAACTAGTATCCCGGGCTCCAGG 60
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 25 AGCTGGAGCTCCACCGCGGCGGCGGCGGCTCTAGAACTAGTATCCCGGGCTCCAGG 84
LI ||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 61 AATTCGGACGAGCGG 76
LI 85 AATTCGGACGAGCGG 100
```

RESULT 27

AAK59576
 ID AAK59576 standard; cDNA: 373 BP.
 XX AC AAK59576;
 XX DT 06-NOV-2001 (first entry)
 XX DE Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:4536.
 XX DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
 KW cytotatic; gene therapy; vaccine; metastasis, ss.
 XX OS Homo sapiens.
 XX PN WO200157182-A2
 XX PD 09-AUG-2001.
 XX PF 17-JAN-2001: 2001WO-0501354
 XX 31-JAN-2000: 2000US-0179065
 PR 04-FEB-2000: 2000US-0180629
 PR 24-FEB-2000: 2000US-0184664
 PR 02-MAR-2000: 2000US-0186359
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 PR 08-NOV-2000: 2000US-0246609
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 PR 08-NOV-2000: 2000US-0246611
 PR 08-NOV-2000: 2000US-0246613
 PR 17-NOV-2000: 2000US-0249307
 PR 17-NOV-2000: 2000US-0249308
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 PR 17-NOV-2000: 2000US-0249310
 PR 17-NOV-2000: 2000US-0249311
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 PR 17-NOV-2000: 2000US-0249318
 PR 17-NOV-2000: 2000US-0249344
 PR 17-NOV-2000: 2000US-0249345
 PR 17-NOV-2000: 2000US-0249364
 PR 17-NOV-2000: 2000US-0249365
 PR 17-NOV-2000: 2000US-0249397
 PR 17-NOV-2000: 2000US-0249399
 PR 17-NOV-2000: 2000US-0249300
 PR 01-DEC-2000: 2000US-0250160
 PR 01-DEC-2000: 2000US-0250391

PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251889.
 PR 08-DEC-2000; 2000US-0251909.
 PR 04-DEC-2000; 2000US-0251900.
 PR 11-DEC-2000; 2000US-0254007.
 PR 05-JAN-2001; 2001US-0259678.
 XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Barash SC, Ruben SM;

XX WPI; 2001-483426/52.

DR P-PSDB; AAM86795.

XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides.
 PT useful for preventing, diagnosing and/or treating cancers and
 PT metastasis.

PS Claim 1: SEQ ID NO 4636; 3071pp + Sequence Listing; English.

XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
 CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patients own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent the
 CC diagnosis and treat metastases of hematopoietic-related diseases, especially
 CC cancers and cancer metastases of hematopoietic-derived cells. AAK4702
 CC to AAK87694 represent human immune/hematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54966 and AAK62160
 CC represent sequences used in the exemplification of the present invention.

XX Sequence 373 BP; 59 A; 129 C; 109 G; 73 T; 3 other.

Query Match 4.2%; Score 75; DB 22; Length 373;
 Best Local Similarity 100.0%; Pred. No. 2e-27;
 Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCATCGCGTGGCGGCGCTCTAGAACTAGTGGATCCGCGGCTGACG 59

Db 19 AGCTGGAGCTCCATCGCGTGGCGGCGCTCTAGAACTAGTGGATCCGCGGCTGACG 59

QY 61 AATTCGGCAGCAGGCC 75

Db 79 AATTCGGCAGCAGGCC 93

RESULT 28

AAK60386

ID AAK60386 standard; cDNA; 411 BP.

XX AC AAK60386;

XX AC AAK60386;

DT 06-NOV-2001 (first entry)

XX Human immune/hematopoietic antigen encoding cDNA SEQ ID NO: 5446

DE Human immune/hematopoietic; immune/hematopoietic antigen; cancer;
 XX cytostatic; gene therapy; vaccine; metastasis; ss.
 KW Human; immune; hematopoietic; immune/hematopoietic antigen; cancer;
 XX cytostatic; gene therapy; vaccine; metastasis; ss.
 XX Homo sapiens

OS

XX

FN W0200157182-A2.
 XX 09-AUG-2001.
 FD 17-JAN-2001; 2001WO-US01354.
 XX 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-0190076.
 PR 18-APR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
 PR 07-JUL-2000; 2000US-0216880.
 PR 11-JUL-2000; 2000US-0217487.
 PR 11-JUL-2000; 2000US-0217496.
 PR 14-JUL-2000; 2000US-0218290.
 PR 26-JUL-2000; 2000US-0220963.
 PR 26-JUL-2000; 2000US-0220964.
 PR 14-AUG-2000; 2000US-0224518.
 PR 14-AUG-2000; 2000US-0224519.
 PR 14-AUG-2000; 2000US-0225213.
 PR 14-AUG-2000; 2000US-0225214.
 PR 14-AUG-2000; 2000US-0225266.
 PR 14-AUG-2000; 2000US-0225267.
 PR 14-AUG-2000; 2000US-0225268.
 PR 14-AUG-2000; 2000US-0225270.
 PR 14-AUG-2000; 2000US-0225447.
 PR 14-AUG-2000; 2000US-0225757.
 PR 14-AUG-2000; 2000US-0225758.
 PR 18-AUG-2000; 2000US-0225759.
 PR 18-AUG-2000; 2000US-0226279.
 PR 22-AUG-2000; 2000US-0226681.
 PR 22-AUG-2000; 2000US-0226868.
 PR 22-AUG-2000; 2000US-0227182.
 PR 23-AUG-2000; 2000US-0227009.
 PR 30-AUG-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0229287.
 PR 01-SEP-2000; 2000US-0229343.
 PR 01-SEP-2000; 2000US-0229344.
 PR 01-SEP-2000; 2000US-0229345.
 PR 05-SEP-2000; 2000US-0229509.
 PR 05-SEP-2000; 2000US-0229513.
 PR 06-SEP-2000; 2000US-0230437.
 PR 06-SEP-2000; 2000US-0230438.
 PR 08-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231244.
 PR 08-SEP-2000; 2000US-0231413.
 PR 08-SEP-2000; 2000US-0231414.
 PR 08-SEP-2000; 2000US-0233080.
 PR 08-SEP-2000; 2000US-0233081.
 PR 12-SEP-2000; 2000US-0231968.
 PR 14-SEP-2000; 2000US-0232397.
 PR 14-SEP-2000; 2000US-0232398.
 PR 14-SEP-2000; 2000US-0232399.
 PR 14-SEP-2000; 2000US-0233400.
 PR 14-SEP-2000; 2000US-0233401.
 PR 14-SEP-2000; 2000US-0233063.
 PR 14-SEP-2000; 2000US-0233064.
 PR 14-SEP-2000; 2000US-0233065.
 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234274.
 PR 25-SEP-2000; 2000US-0234597.
 PR 25-SEP-2000; 2000US-0234998.
 PR 26-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235834.
 PR 27-SEP-2000; 2000US-0235836.

PI Rosen CA, Ruben SM, Komatsoulis G;
 XX WPI: 2000-511712-70
 DR P-PSDB; AAB45169.
 XX
 XX Nucleic acid molecules encoding human secreted proteins, used in
 PT preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
 PT Parkinson's diseases and cancers -
 XX
 XX Claim 4: Page 380; 44Opp: English.
 XX
 XX Polynucleotide sequences AAC80531-C80580 represent cDNA encoding human
 CC secreted proteins AAB45170-B45225. Sequences AAB45170-B45225 represent
 CC alternative polypeptides encoded by the genes, and amino acid sequences
 CC to which they are homologous. The genes and proteins have activities
 CC dependent on the tissues and cells in which they are expressed. Examples
 CC of their activities include immunosuppressive; antiarthritic; XX
 CC antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
 CC cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide;
 CC fungicide, and ophthalmological. The secreted proteins, polypeptides, XX
 CC antagonists and agonists may be useful in treating, preventing and/or
 CC diagnosing diseases and disorders such as autoimmune diseases
 CC e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms
 CC of the breast or liver, cardiovascular disorders e.g. cardiac arrest,
 CC cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous
 CC system disorders e.g. Alzheimer's disease, infections caused by
 CC bacteria, viruses and fungi and ocular disorders e.g. corneal infection.
 CC The polypeptides can also be used to aid wound healing and epithelial
 CC cell proliferation, to prevent skin aging due to sunburn, to maintain
 CC organs before transplantation, for supporting cell culture of primary
 CC tissues, to regenerate tissues and in chemotaxis. The polypeptides can
 CC also be used as a food additive or preservative to increase or decrease
 CC storage capabilities. AAC80522-C80530 and AAB45119 represent sequences
 CC used in the isolation and characterisation of the genes and proteins of
 CC the invention.
 XX
 XX Sequence 558 BP; 107 A, 147 C, 169 G, 130 T; 5 other;
 XX
 XX Query Match 4.2%; Score 75; DB 21; Length 558;
 XX Best Local Similarity 100.0%; Pred. No. 2e-27;
 XX Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
 QY 1 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGCGGTGCAGG 60
 DB 54 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGCGGTGCAGG 113
 QY 61 AATTCGGCAGGAGCC 75
 DB 114 AATTCGGCAGGAGCC 128
 RESULT 30
 AAA87692
 ID AAA87692 standard; cDNA; 745 BP.
 XX
 XX AAA87692;
 XX
 XX 04-DEC-2000 (first entry)
 XX
 XX Human secreted protein gene 27 SEQ ID NO:37.
 XX
 XX Human; secreted protein; immunosuppressive, immunostimulant, neurotropic;
 FW antiinflammatory; cardiant; vulnerary; antiulcer; anticonvulsant;
 KW antiparkinsonian; neuroprotective; antiviral; antibacterial; cytostatic;
 KW antiparasitic; thrombolytic; anticoagulant; antiarteriosclerotic;
 KW gene therapy; vaccine; chemotaxis-modulator; angiogenesis-modulator;
 KW cancer; immune system disorder; hyperproliferative disorder; infection;
 KW cardiovascular disorder; neurological disease; wound healing; ss.
 XX
 XX Homo sapiens.
 XX
 XX W0200043495-A2.
 XX
 XX

27-JUL-2000.
 18-JAN-2000, 2000WO-US00903.
 19-JAN-1999; 99US-0116330.
 (HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Ruben SM, Ebner R, Young PE, Ni J, Moore PA;
 Komatsoulis G, Birse CE;
 WPI: 2000-499225/44.
 P-PSDB, AAB25691.
 New isolated polynucleotide encoding a secreted protein useful for
 preventing, treating or ameliorating a medical condition -
 Claim 1; Page 394; 45lpp: English.
 The polynucleotide sequences given in AAA87665 to AAA87708 encodes the
 human secreted proteins given in AAB25665 to AAB25755. Human secreted
 proteins have activities based on the tissues and cells the genes are
 expressed in. Examples of activities include: immunosuppressive;
 immunostimulant; antiinflammatory; cardiant; vulnerary; antiulcer;
 neurotropic; antiviral; anticonvulsant; antiparkinsonian; neuroprotective;
 antibacterial; antiparasitic; thrombolytic; anticoagulant;
 antiarteriosclerotic and cytostatic. The secreted proteins and their
 polynucleotides can be used in gene therapy and as vaccines,
 chemotaxis-modulators and angiogenesis- modulators. The human secreted
 proteins and polynucleotides can be used for diagnosing (the
 susceptibility to) a pathological condition by determining the presence
 or absence of a mutation in the polynucleotide or determining the
 presence or amount of expression of the protein. The polynucleotides and
 proteins can also be used in the treatment and diagnosis of cancer,
 diseases of the immune system, hyperproliferative disorders,
 cardiovascular disorders and neurological disease. They can also be used
 to promote wound healing and to fight infection. AAA87657 to AAA87665 and
 AAB25664 represent sequences used in the exemplification of the present
 invention.
 Sequence 745 BP, 191 A, 214 C, 188 G, 142 T; 10 other;
 Query Match 4.2%; Score 75; DB 21; Length 745;
 Best Local Similarity 100.0%; Pred. No. 2e-27;
 Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
 QY 1 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGCGGTGCAGG 60
 DB 327 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGCGGTGCAGG 386
 QY 61 AATTCGGCAGGAGCC 75
 DB 387 AATTCGGCAGGAGCC 401
 RESULT 31
 ABA12886
 ID ABA12886 standard; cDNA; 829 BP.
 XX
 XX ABA12886;
 XX
 XX 23-JAN-2002 (first entry)
 XX
 XX Human nervous system related polynucleotide SEQ ID NO 1893.
 XX
 XX Human; neurotropic; neuroprotective; cytostatic; dermatological; virucide;
 KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
 KW antiparkinsonian; antiskickling; antianaemic; antiarthritic; cancer;
 KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
 KW antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
 KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ss.
 XX
 XX

OS	Homo sapiens.		
XX	WC200159063-A2		
XX	16-AUG-2001		
PD			
XX			
PP	17-JAN-2001	2500US-0119065	2500US-0119065
XX			
PP	31-JAN-2000	2000US-0119065	2000US-0119065
PP	04-FEB-2000	2000US-0180528	2000US-0180528
PP	24-FEB-2000	2000US-0184164	2000US-0184164
PP	02-MAR-2000	2000US-0186350	2000US-0186350
PP	16-MAR-2000	2000US-0189874	2000US-0189874
PP	17-MAR-2000	2000US-0190076	2000US-0190076
PP	18-APR-2000	2000US-0198123	2000US-0198123
PP	19-MAY-2000	2000US-0205515	2000US-0205515
PP	07-JUN-2000	2000US-0209467	2000US-0209467
PP	28-JUN-2000	2000US-0214285	2000US-0214285
PP	30-JUN-2000	2000US-0215135	2000US-0215135
PP	07-JUL-2000	2000US-0216647	2000US-0216647
PP	07-JUL-2000	2000US-0216648	2000US-0216648
PP	11-JUL-2000	2000US-0217487	2000US-0217487
PP	11-JUL-2000	2000US-0217496	2000US-0217496
PP	14-JUL-2000	2000US-0218290	2000US-0218290
PP	26-JUL-2000	2000US-0220363	2000US-0220363
PP	26-JUL-2000	2000US-0220464	2000US-0220464
PP	14-AUG-2000	2000US-0224518	2000US-0224518
PP	14-AUG-2000	2000US-0224519	2000US-0224519
PP	14-AUG-2000	2000US-0225213	2000US-0225213
PP	14-AUG-2000	2000US-0225214	2000US-0225214
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PP	14-AUG-2000	2000US-0225267	2000US-0225267
PP	14-AUG-2000	2000US-0225268	2000US-0225268
PP	14-AUG-2000	2000US-0225270	2000US-0225270
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PP	14-AUG-2000	2000US-0225759	2000US-0225759
PP	18-AUG-2000	2000US-0226279	2000US-0226279
PP	22-AUG-2000	2000US-0226681	2000US-0226681
PP	22-AUG-2000	2000US-0226688	2000US-0226688
PP	22-AUG-2000	2000US-0227182	2000US-0227182
PP	23-AUG-2000	2000US-0227009	2000US-0227009
PP	30-AUG-2000	2000US-0228924	2000US-0228924
PP	01-SEP-2000	2000US-0229267	2000US-0229267
PP	01-SEP-2000	2000US-0229444	2000US-0229444
PP	01-SEP-2000	2000US-0229344	2000US-0229344
PP	01-SEP-2000	2000US-0229345	2000US-0229345
PP	05-SEP-2000	2000US-0229509	2000US-0229509
PP	05-SEP-2000	2000US-0229513	2000US-0229513
PP	06-SEP-2000	2000US-0230437	2000US-0230437
PP	06-SEP-2000	2000US-0230438	2000US-0230438
PP	08-SEP-2000	2000US-0231242	2000US-0231242
PP	08-SEP-2000	2000US-0231413	2000US-0231413
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PP	08-SEP-2000	2000US-0231414	2000US-0231414
PP	08-SEP-2000	2000US-0231980	2000US-0231980
PP	08-SEP-2000	2000US-0231981	2000US-0231981
PP	12-SEP-2000	2000US-0231968	2000US-0231968
PP	14-SEP-2000	2000US-0232397	2000US-0232397
PP	14-SEP-2000	2000US-0232398	2000US-0232398
PP	14-SEP-2000	2000US-0232399	2000US-0232399
PP	14-SEP-2000	2000US-0232400	2000US-0232400
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PP	14-SEP-2000	2000US-0234064	2000US-0234064
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PP	25-SEP-2000	2000US-0234997	2000US-0234997
PP	25-SEP-2000	2000US-0234998	2000US-0234998
PP	26-SEP-2000	2000US-0235484	2000US-0235484
XX			
PA	(HUMA-) HUMAN GENOME SCI INC.		

PR 18-AUG-2000; 2000US-0226279
 PR 22-AUG-2000; 2000US-0226581
 PR 22-AUG-2000; 2000US-0226668
 PR 22-AUG-2000; 2000US-0227192
 PR 22-AUG-2000; 2000US-0227604
 PR 30-AUG-2000; 2000US-0228924
 PR 30-AUG-2000; 2000US-0229087
 PR 01-SEP-2000; 2000US-0229387
 PR 01-SEP-2000; 2000US-0229343
 PR 01-SEP-2000; 2000US-0229344
 PR 01-SEP-2000; 2000US-0229445
 PR 04-SEP-2000; 2000US-0229404
 PR 05-SEP-2000; 2000US-0229413
 PR 06-SEP-2000; 2000US-0230437
 PR 06-SEP-2000; 2000US-0230438
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 PR 02-OCT-2000; 2000US-0237037
 PR 02-OCT-2000; 2000US-0237038
 PR 02-OCT-2000; 2000US-0237039
 PR 02-OCT-2000; 2000US-0237040
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 PR 20-OCT-2000; 2000US-0241826
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PR 08-NOV-2000; 2000US-0246613
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 PR 17-NOV-2000; 2000US-0249299
 PR 01-DEC-2000; 2000US-0250160
 PR 01-DEC-2000; 2000US-0250391
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 PR 05-DEC-2000; 2000US-0251988
 PR 05-DEC-2000; 2000US-0256719
 PR 06-DEC-2000; 2000US-0251479
 PR 08-DEC-2000; 2000US-0251856
 PR 08-DEC-2000; 2000US-0251868
 PR 08-DEC-2000; 2000US-0251869
 PR 08-DEC-2000; 2000US-0251989
 PR 08-DEC-2000; 2000US-0251990
 PR 11-DEC-2000; 2000US-0254097
 PR 05-JAN-2001; 2001US-0259678

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-465572/50.

F-SDDB, AAU19797.

Nucleic acid molecules encoding human secreted extracellular matrix proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers -

Claim 1. SEQ ID NO 182, 577pp. English.

The invention relates to isolated nucleic acid molecules encoding novel human secreted extracellular matrix proteins (SPs). The polynucleotides and proteins are used to prevent, treat a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. For example, disorders associated with decreased expression of SPs. The SP polynucleotide or a vector expressing them may be administered to treat diseases by gene therapy. Antisense molecules may be administered to down regulate expression of SPs by binding with the cells own genes and preventing their expression. The polynucleotides may also be used as tNA probes in diagnostic assays. The SPs may also be used as antigens to produce antibodies and to identify modulators (agonists and antagonists) of the SPs. The anti-(SP) antibodies and antagonists may also be used to down regulate expression and activity of SP and as diagnostic agents for detecting the presence of SPs in samples. The disorders include for example: immune/autoimmune diseases (e.g. HIV (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis and multiple sclerosis), cancers and hyperproliferative disorders (e.g. melanomas, neoplasms of the breast or liver, Sezary syndrome and Gaucher's disease), neurological diseases (e.g. Alzheimer's disease, Parkinson's disease), cardiac/cerebrovascular disorders (e.g. cardiac arrest, tachycardia and angina), infections caused by bacteria, viruses and fungi and ocular disorders (e.g. corneal infections). Other uses include wound healing, maintenance of organs before transplantation,

Query Match 4 29; Score 75; DB 22; Length 1355;
 Best Local Similarity 100.0%; Pred. No. 2e-27;

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Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
QY 1 AGCTGAGACTGACAGCGGGTGGCGGCTCTAGAACTAGTGGATGATCCCGGCTGACG 60
    |||||||
Db 911 AGCTGAGACTGACAGCGGGTGGCGGCTCTAGAACTAGTGGATGATCCCGGCTGACG 852
QY 61 AATTGGCAGCAGGC 75
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RESULT 40
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DT 04-DEC-2001 (first entry)
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DE cDNA encoding novel human neoplastic disease associated polypeptide #244.
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KW Human; neoplastic disease associated polypeptide; cancer; gene therapy;
KW hyperproliferative disorder; neural disorder; immune system disorder;
KW muscular disorder; reproductive disorder; gastrointestinal disorder;
KW pulmonary disorder; cardiovascular disorder; renal disorder;
KW neuroprotective; cytostatic; anti inflammatory; vasotropic; ss.
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OS Homo sapiens
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PD 02-AUG-2001
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11-DEC-2000, 2000US-0254097.
 05-JAN-2001, 2001US-0259678.
 (HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Barash SC, Ruben SM;
 WPI, 2001-465577/50.
 F-PSDB: AAU07602.
 Nucleic acid molecules encoding tumour necrosis factor ligands, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's disease and rheumatoid arthritis -
 Claim 1; SEQ ID NO 13, 436pp; English!
 Tumour necrosis factor receptor-like (TNFR-like) polypeptides and their associated polynucleotides of the invention are useful in the diagnosis, treatment and prevention of various types of disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A pathological condition can be determined by determining the presence or absence of a mutation in a TNFR-like polynucleotide. The treatable disorders include autoimmune diseases such as rheumatoid arthritis, hyperproliferative disorders such as neoplasms of the breast or liver, cardiovascular disorders such as cardiac arrest, cerebrovascular disorders such as cerebral ischaemia, nervous system disorders such as Alzheimer's disease, infections caused by bacteria, viruses and fungi, ocular disorders such as corneal infection, endocrine disorders such as Cushing's Syndrome, gastrointestinal disorders such as Crohn's disease, renal disorders such as glomerulonephritis and respiratory disorders such as asthma. The polypeptides can also be used to aid wound healing, to prevent skin aging due to sunburn, to maintain organs before transplantation, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. This sequence represents a TNFR-like cDNA polynucleotide of the invention.
 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO

Query Match 4.2%, Score 75, DB 12, Length 1591;
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 Matches 75, Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 61 AATTGGGCGAGGCGC 75
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RESULT 43
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 DT 15-AUG-2000 (first entry)
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 KW Adipose specific protein 1; ASP-1, apoptosis, obesity, hypertension.
 KW Cardiovascular disorder; arteriosclerosis; diabetes; anorexia;
 KW hyperglycaemia, hyperglycaemia, human, fat specific protein, FSP27, ds.
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Rosen CA, Barash SC, Ruben SM;
WFI; 2001-465460/50.
F-PSDB; AAU17387.

Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune disorders and neuronal disorders.

Claim 1; SEQ ID No 339; 880pp; English.

The invention relates to novel isolated polypeptides (I), and polynucleotides (II). (I), (II) and the antibody to (I) are useful for diagnosing, preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ transplant rejections and graft versus host disease, infectious diseases (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and other blood-related disorders (sickle cell anaemia), myeloproliferative disorders, primary haematopoietic disorders, hyperproliferative disorders (e.g. Gaucher's disease and cancer), neurodegenerative disorders (e.g. Alzheimer's disease, Parkinson's disease), chromosomal abnormalities (Down syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g. glomerulonephritis), cardiovascular disorders (e.g. arrhythmia), respiratory disorders, dermatological disorders, in wound healing, epithelial cell proliferation, endocrine disorders (e.g. Addison's disease), reproductive system disorders, gastrointestinal disorder (inflammatory disorders), liver disorders (cirrhosis), cancer (inflammatory disorders), cell responsiveness to pathogens, activators of tumour proliferation in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAS26976-AAS27850 represent novel signal transduction pathway protein coding regions and PCR primers of the invention.

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DD 04-NOV-1980

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 PR 11-DEC-2000: 2000US-0254097
 PR 01-JAN-2001: 2000US-0254678

(HUMA-) HUMAN GENOME SCI INC.
 Posen CA, Barash SC, Puben SM;
 WFLI, 2001-465570/50.

Isolated nucleic acid molecule encoding a reproductive system antigen -
 is used in preventing, treating or ameliorating a medical condition -
 Disclosure, SEQ ID NO 2662, 1297pp + Sequence Listing, English.

08-NOV-2000: 2000US-0246610.
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 PR 11-DEC-2000: 2000US-0254007.
 PR 05-JAN-2001: 2001US-0259678.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 DX WPI: 2001-483232/52.
 XX
 PT Nucleic acids encoding 973 human testicular antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating testicular cancer -
 PS
 Claim 1: SEQ ID NO 990, 766pp, English.
 XX
 CC The present invention provides the protein and coding sequences of 973
 CC human testicular antigens, and fragments of their genomic sequences. The
 CC sequences can be used in the treatment of cardiovascular, urinary system,
 CC reproductive system, immune, respiratory, neurological and
 CC gastrointestinal disorders, infections, and particularly cancer,
 CC especially testicular cancers. The present sequence is a cDNA of the
 CC invention.
 XX
 SQ Sequence 2099 BP; 499 A; 587 C; 516 G; 487 T; 10 other;

Query Match 4.2%; Score 75; DB 23; Length 2099;
 Best Local Similarity 100.0%; Pred. No. 2e-27;
 Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGCTGGAGCTCCACCGGCTGGGGCTCTAGAACTAGTGGATCCCGGGCTCCAGG 46
 DB 393 AGCTGGAGCTCCACCGGCTGGGGCTCTAGAACTAGTGGATCCCGGGCTCCAGG 452
 QY 61 AATTGGGACAGGAGC 75
 DB 453 AATTGGGACAGGAGC 467

RESULT 49
 AAH35162
 ID AAH35162 standard; cDNA: 200 BP.

XX AAH35162;
 XX 03-SEP-2001 (first entry)
 DE Human colon cancer antigen encoding cDNA SEQ ID NO:2244.
 XX
 KW Human, colon cancer, colon cancer antigen, diagnosis; detection;
 KW colorectal carcinoma; ss.
 US Homo sapiens.
 XX WJ20012920-A2.
 XX 05-APR-2001.
 XX 28-SEP-2000: 2000WO-US26524.
 XX 29-SEP-1999: 99US-0157137.
 XX 03-NOV-1999: 99US-0163280.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Ruben SM, Barash SC, Birse CE, Rosen CA;
 XX WPI: 2001-235357/24.
 XX P-PSDB: AAG75757.
 XX
 PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
 PT useful for preventing, diagnosing and/or treating colorectal cancers -
 XX
 Claim 1, Page 3747, 9803pp, English.
 XX
 CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where
 CC the proteins are collectively known as colon cancer antigens. The colon
 CC cancer antigens have cytostatic activity and can be used in gene
 CC therapy and vaccine production. N and P may be used in the prevention,
 CC diagnosis and treatment of diseases associated with inappropriate P
 CC expression. For example, N and P may be used to treat disorders
 CC associated with decreased expression by rectifying mutations or deletions
 CC in a patient's genome that affect the activity of P by expressing
 CC inactive proteins or to supplement the patients own production of P.
 CC Additionally, N may be used to produce the colon cancer-associated Ps,
 CC by inserting the nucleic acids into a host cell and culturing the cell
 CC to express the proteins. N and P can be used in the prevention, diagnosis
 CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
 CC and AAH77789 represent sequences used in the exemplification of the
 CC present invention.
 CC R.N. Pages 666 to 682 and page 7053 of the sequence listing were
 CC missing at time of publication, meaning no sequences are present for
 CC SEQ ID NO:1027 to 1052, 7921 and 7922.
 XX
 SQ Sequence 200 BP; 40 A; 62 C; 57 G; 31 T; 10 other;

Query Match 4.2%; Score 74; DB 22; Length 200;
 Best Local Similarity 100.0%; Pred. No. 6.4e-27;
 Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 47 AGCTGGAGCTCCACCGGCTGGGGCTCTAGAACTAGTGGATCCCGGGCTCCAGG 106
 QY 61 AATTGGGACAGGAGC 74
 DB 107 AATTGGGACAGGAGC 120

RESULT 50
 AAH35170
 ID AAH35170 standard; cDNA: 247 BP.
 XX
 AC AAH35170;

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 31, 2002, 11:13.10 , Search time 63 seconds
(without alignments)
9381 217 Million cell updates/sec

Title: us-09-854-300-7

Perfect score: 1774

Sequence: 1 agctgagctccaccgcggt. ataggcaattctctctcaq 1774

Scoring table:

OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 310279 seqs, 166577418 residues

Word size : 0

Total number of hits satisfying chosen parameters: 620558

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Database : Published_Applications_NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	704	39.7	1250	10	US-09-764-864-519
3	275	15.5	643	9	US-10-046-935-1815
4	186	10.5	340	10	US-09-783-590-3523
5	167	9.4	435	10	US-09-920-300A-1176
6	167	9.4	435	12	US-10-033-528-1176
7	80	4.5	922	10	US-09-800-729-23
8	76	4.3	1772	10	US-09-764-853-148
9	72	4.2	1355	10	US-09-764-870-192
10	74	4.2	496	10	US-09-764-853-404
11	74	4.2	640	10	US-09-908-711-28
12	74	4.2	737	10	US-09-764-853-172
13	74	4.2	791	10	US-09-764-853-305
14	74	4.2	796	10	US-09-764-853-365
15	74	4.2	852	10	US-09-764-864-60
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17	74	4.2	1190	10	US-09-764-898-123
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19	74	4.2	1454	10	US-09-764-864-9

20	74	4.2	1707	10	US-09-764-870-217	Sequence 217, App
21	74	4.2	1788	10	US-09-764-898-40	Sequence 40, Appl
22	74	4.2	2005	10	US-09-764-903-22	Sequence 22, Appl
23	74	4.2	2458	10	US-09-764-864-78	Sequence 78, Appl
24	73	4.1	367	10	US-09-764-860-248	Sequence 248, App
25	73	4.1	421	10	US-09-764-855-67	Sequence 67, Appl
26	73	4.1	604	10	US-09-925-301-619	Sequence 619, App
27	73	4.1	618	10	US-09-764-853-136	Sequence 136, App
28	73	4.1	618	10	US-09-764-853-377	Sequence 377, App
29	73	4.1	618	10	US-09-764-898-126	Sequence 126, App
30	73	4.1	631	10	US-09-908-711-29	Sequence 29, Appl
31	73	4.1	647	10	US-09-764-898-84	Sequence 84, Appl
32	73	4.1	771	10	US-09-764-887-129	Sequence 129, App
33	73	4.1	869	10	US-09-764-864-289	Sequence 289, App
34	73	4.1	975	10	US-09-789-561-58	Sequence 58, Appl
35	73	4.1	1066	10	US-09-764-898-54	Sequence 54, Appl
36	73	4.1	1427	10	US-09-925-300-639	Sequence 639, App
37	73	4.1	1511	10	US-09-764-853-308	Sequence 308, App
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41	73	4.1	1637	10	US-09-925-300-770	Sequence 770, App
42	73	4.1	1737	10	US-09-863-027-13	Sequence 13, Appl
43	73	4.1	1906	10	US-09-739-254-32	Sequence 32, Appl
44	73	4.1	1906	10	US-09-904-615-32	Sequence 32, Appl
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47	73	4.1	2330	10	US-09-764-853-189	Sequence 189, App
48	73	4.1	2596	10	US-09-764-853-380	Sequence 380, App
49	73	4.1	2596	10	US-09-764-898-128	Sequence 128, App
50	73	4.1	2751	10	US-09-789-561-64	Sequence 64, Appl
51	73	4.1	2787	10	US-09-764-864-412	Sequence 412, App
52	73	4.1	2919	10	US-09-764-870-94	Sequence 94, Appl
53	73	4.1	3328	10	US-09-838-539-1	Sequence 1, Appl
54	72	4.1	439	10	US-09-925-299-484	Sequence 484, App
55	71	4.0	2045	10	US-09-861-270-1	Sequence 1, Appl
56	70	3.9	570	10	US-09-734-017A-7	Sequence 7, Appl
57	68	3.8	835	10	US-09-764-864-245	Sequence 245, App
58	68	3.8	1169	10	US-09-839-645-1	Sequence 1, Appl
59	66	3.7	344	10	US-09-924-035A-864	Sequence 864, App
60	66	3.7	752	10	US-09-956-004-108	Sequence 108, App
61	66	3.7	1712	10	US-09-925-300-643	Sequence 643, App
62	65	3.7	328	10	US-09-925-400-574	Sequence 574, App
63	65	3.7	503	10	US-09-764-847-380	Sequence 380, App
64	65	3.7	799	10	US-09-911-826A-3	Sequence 3, Appl
65	65	3.7	836	10	US-09-764-853-393	Sequence 393, App
66	65	3.7	1409	10	US-09-925-301-176	Sequence 176, App
67	65	3.7	1753	10	US-09-764-864-774	Sequence 774, App
68	65	3.7	2082	9	US-09-990-046-9	Sequence 9, Appl
69	65	3.7	2554	10	US-09-764-864-352	Sequence 352, App
70	65	3.7	3348	10	US-09-954-456-90	Sequence 90, Appl
71	65	3.7	3348	10	US-09-954-456-727	Sequence 727, App
72	64	3.6	726	10	US-09-954-456-727	Sequence 201, App
73	63	3.6	100	10	US-09-954-456-727	Sequence 19, Appl
74	63	3.6	624	10	US-09-840-728A-19	Sequence 469, App
75	63	3.6	1175	10	US-09-834-975-469	Sequence 286, App

ALIGNMENTS

RESULT 1
US-09-764-864-43
Sequence 63, Application US/09764864
Patent No. US20020132753A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT223
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1792

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 2306
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09;764-864-63

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Query Match		45.4%	Score 824	DB 10	Length 2306
Best Local Similarity		99.6%	Prd No. 0		
Matches 1144:	Conservative	0	Mismatches	4	Indels 1: Gaps 1:
Qy	547	CTTTAACTGGGAAAGAAATTTACGGSTGCTGAGTGGTGGTGGGAGGACATGCTGAATATC	K06		
Db	12	CTGTACCGGACATAGAAATTTACGGSTGCTGAGTGGTGGTGGGAGGACATGCTGAATATC	71		
Qy	607	TTGGTTGGGCGCTCATCCAAACGGGGGGGGGCTGCACCTTCCACACAAGATCCATCTGGC	131		
Db	72	TTGGTTGGGCGCTCATCCAAACGGGGGGGGGCTGCACCTTCCACACAAGATCCATCTGGC	131		
Qy	667	TTATGAGAGATGGGCGCTGGAGCGCTCATCTTTAACTTCCCGGACATCGATGATG	726		
Db	132	TTATGAGAGAGGGGCGCTGGAGCGCTCATCTTTAACTTCCCGGACATCGATGATG	141		
Qy	727	CATCCCCATGCTCTCACCCGGGTGCAGTAGACATGTTGCCAATCATGATCGCAATCTGAA	786		
Db	192	CATCCCCATGCTCTCACCCGGGTGCAGTAGACATGTTGCCAATCATGATCGCAATCTGAA	251		
Qy	787	AGGACACAAAATCTGCCATCTATTCAAGAGCGCATCAAGTCGACATGCTGATAGAAAT	846		
Db	252	AGGACACAAAATCTGCCATCTATTCAAGAGCGCATCAAGTCGACATGCTGATAGAAAT	311		
Qy	847	AGGAAAAAACATGCGCTTGGTGAATCAATCAATTTAAATTTTGTGTGTGTGTGTGTGT	905		
Db	312	AGGAAAAAACATGCGCTTGGTGAATCAATCAATTTAAATTTTGTGTGTGTGTGTGTGT	371		
Qy	906	TTTTTTATTATAGGGGGGAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	965		
Db	372	TTTTTTATTATAGGGGGGAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	431		
Qy	966	GGAAATCAACATCTAAAGTCAGGAGGAGAGGAAATAAGAGAGATGCTGATGAAAAAGCTA	1025		
Db	432	GGAAATCAACATCTAAAGTCAGGAGGAGAGGAAATAAGAGAGATGCTGATGAAAAAGCTA	491		
Qy	1026	TTGGAAATCTTAACTAGGATCAATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1085		
Db	492	TTGGAAATCTTAACTAGGATCAATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	551		
Qy	1086	ATAGT	1145		
Db	552	ATAGT	611		
Qy	1146	GCAACCATATTTCCATTAAGACATGTTGTGATGATGATGATGATGATGATGATGATGATG	1205		
Db	612	GCAACCATATTTCCATTAAGACATGTTGTGATGATGATGATGATGATGATGATGATGATG	671		
Qy	1206	CTATGTGAAATCTAAATATTAAGATTTTGGAAATGATGATGATGATGATGATGATGATGAT	1265		
Db	672	CCATGTGCAATATGACATCTCAAAGTTTGGAAATGATGATGATGATGATGATGATGATGAT	731		
Qy	1266	CATGTGTTTAAATCTGCTGTATGCAATGAATATTAATATGATGATGATGATGATGATGATG	1325		
Db	732	CATGTGTTTAAATCTGCTGTATGCAATGAATATTAATATGATGATGATGATGATGATGATG	791		
Qy	1326	AGGATATGCAAGGAG	1385		
Db	792	AGGATATGCAAGGAG	851		
Qy	1386	CGGCTGTGAGGAG	1445		
Db	852	CGGCTGTGAGGAG	911		
Qy	1446	CAATGCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1505		

```

RESULT 2
US-09-764-864-519
; Sequence 519, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: Ptz23
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 519
; LENGTH: 1250
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (540)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1242)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-764-864-519

```

Query Match	99.74%	Score 704	DB 10	Length 1250
Best Local Similarity	99.54%	Pred. No. 0		
Matches 1144	Conservative	0	Mismatches 4	Indels 2
				Caps
QY	547	CTSTAAACCGGCACACGAATTTACGGGTGGCCACAGGTTTTGGGCAAGCACCGCTGCAAGTCTC	606	
DB	18	CTGTAAACCGGCACACGAATTTACGGGTGGCCACAGGTTTTGGGCAAGCACCGCTGCAAGTCTC	77	
QY	607	TTGGTGTGGGCTGTCATCTCAAGCAAGCGCGGGGGGCTGTACCTTTGTGACACAAAGATGCCATCTGGC	666	
DB	74	TTGGTGTGGGCTGTCATCTCAAGCAAGCGCGGGGGGCTGTACCTTTGTGACACAAAGATGCCATCTGGC	137	
QY	667	TTATGAGACATGCGGGGCTCTTGAGAGCGCTGTATCTTTAACTTTCCCGGACCCGCCAATGAGGT	726	
DB	148	TTATGAGACAGGGGGGCTCTTGAGAGCGCTGTATCTTTAACTTTCCCGGACCCGCCAATGAGGT	197	
QY	727	CATCCGCGCATGTCTTACCTGGGGGCTGGCATAGACATGTGTGTCAATCATGATCGGCAATCTGAA	786	
DB	148	CATCCGCGCATGTCTTACCTGGGGGCTGGCATAGACATGTGTGTCAATCATGATCGGCAATCTGAA	257	
QY	787	AGGCAACAAAATTTGTCAATTTATTGAAAAGAGCATACAAAGTGCATTAATGGTCATAGAAAT	848	
DB	258	AGGCAACAAAATTTGTCAATTTATTGAAAAGAGCATACAAAGTGCATAGAAAT	317	
QY	847	AGGCAAAAAAACATGGGCTTTGGGTTGAATCACTATTTCAAATTTTTTTGTTCTCTGTGTCT	905	
DB	318	AGGCAAAAAAACATGGGCTTTGGGTTGAATCACTATTTCAAATTTTTTTGTTCTCTGTGTCT	377	

QY 906 TTTTATTATTACGGCGCAACTGTGGGTATTTTATCTTTTATCTGTCGAAGCTAC 965
Db 378 TTTTATTATTACGGCGCAACTGTGGGTATTTTATCTTTTATCTGTCGAAGCTAC 437
QY 966 GGAATGGAAGCTCAAGCAGGAGCAGAGGCAATTAAGGCGAGATGCTAAAAAGCTA 1025
Db 438 GGAATGGAAGCTCAAGCAGGAGCAGAGGCAATTAAGGCGAGATGCTAAAAAGCTA 497
QY 1026 TTGAAGGCTTCAACTACGACACTGAAACAGGAGAGCAAGG-AAAATGGGCTGATGGA 1084
Db 498 TTGAAGGCTTCAACTACGACACTGAAACAGGAGAGCAAGG-AAAATGGGCTGATGGA 557
QY 1085 GATAGTGTGCTGTGTCATGTAATGTATTAACCAAAATGATTTGGTAGCATCTTAAG 1144
Db 558 GATAGTGTGCTGTGTCATGTAATGTATTAACCAAAATGATTTGGTAGCATCTTAAG 617
QY 1145 TGCACCAATATTTTCCATAAGACATGTTGACCCCATGGGTGTAAACACAGAGCTGC 1204
Db 618 TGCACCAATATTTTCCATAAGACATGTTGACCCCATGGGTGTAAACACAGAGCTGC 677
QY 1205 CCCATGTGTAATGTGACATACTCAAGGCTTTGGGAAATTCAGGAGGAGATGGA 1264
Db 678 CCCATGTGTAATGTGACATACTCAAGGCTTTGGGAAATTCAGGAGGAGATGGA 737
QY 1265 TCAGTGTCTTACAGTCCCTGTATCCAATGAATATCTAATAGTGCCTCCCTCCCATGAA 1324
Db 738 TCAGTGTCTTACAGTCCCTGTATCCAATGAATATCTAATAGTGCCTCCCTCCCATGAA 797
QY 1325 GAGGATAATCTGATGAGATGATCATCTGATATGTTTCAATAGGAGGAGACAGATGAA 1384
Db 798 GAGGATAATCTGATGAGATGATCATCTGATATGTTTCAATAGGAGGAGACAGATGAA 857
QY 1385 CCGGCTCTGGAGGAGACAGGCTGAGTCAACAAATGAAAGTCTAGAGGAGGAGAGATGAA 1444
Db 858 CCGGCTCTGGAGGAGACAGGCTGAGTCAACAAATGAAAGTCTAGAGGAGGAGAGATGAA 917
QY 1445 GCAATTTGATGAGTGTATGATCTGATGATGATGATGATGATGATGATGATGATGAT 1504
Db 918 GCAATTTGATGAGTGTATGATCTGATGATGATGATGATGATGATGATGATGATGAT 977
QY 1505 GAACTCTTAATCAAGGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1564
Db 978 GAACTCTTAATCAAGGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1027
QY 1565 AARACTGAGCATTAATATACAGAGATGATGATGATGATGATGATGATGATGATGATGAT 1624
Db 1038 AARACTGAGCATTAATATACAGAGATGATGATGATGATGATGATGATGATGATGATGAT 1097
QY 1625 TTGATAAAATTAATAAATAAGAGTGTATGATGATGATGATGATGATGATGATGATGAT 1684
Db 1098 TTGATAAAATTAATAAATAAGAGTGTATGATGATGATGATGATGATGATGATGATGAT 1157
QY 1685 TATAGTTAAA 1694
Db 1158 TATAGTTAAA 1167

RESULT 3

US-10-046-935-1815
; Sequence 1815, Application US/10046935
; Patent No. US20020156011A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secrist, Heather
; APPLICANT: Wang, Aijun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.527C1
; CURRENT APPLICATION NUMBER: US/10/046.935
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 2229

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1815
; LENGTH: 643
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 584
; OTHER INFORMATION: n = A,T,C or G
US-10-046-935-1815

Query Match 15.5%; Score 275; DB 9; Length 643;

Best Local Similarity 99.7%; Pred No 3 Ke-132;
Matches 325; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1369 ACAGGGAACAGATGAACCGGCTCTGGAGGAACAGTGGCACTCAACAAATGAAAGTCTACA 1428
Db 1 ACAGGGAACAGATGAACCGGCTCTGGAGGAACAGTGGCACTCAACAAATGAAAGTCTACA 60
QY 1429 GCTGGTAAACCATGAAGCAAAATCTCTGGCAGTGGATGTTATCTCTCATGTGACAAACC 1488
Db 61 GCTGGTAAACCATGAAGCAAAATCTCTGGCAGTGGATGTTATCTCTCATGTGACAAACC 120
QY 1489 AACCTTTGAAGAGACAGAACTCCTAATCAAGAGACTGCTGTTCGAGAAATTAATCTTA 1548
Db 121 AACCTTTGAAGAGACAGAACTCCTAATCAAGAGACTGCTGTTCGAGAAATTAATCTTA 180
QY 1549 AAATCTGTAAATAGAAAACCTTGAACCATTAAGTAATAACAGAACTGCCAATCAGGGCT 1608
Db 181 AAATCTGTAAATAGAAAACCTTGAACCATTAAGTAATAACAGAACTGCCAATCAGGGCT 240
QY 1609 AGTTCTTATTAAATTTGGATAAATTTAATAAATAAGAGTACTGAAAGTCTCAG 1668
Db 241 AGTTCTTATTAAATTTGGATAAATTTAATAAATAAGAGTACTGAAAGTCTCAG 300
QY 1669 ATGACTAATATTATGCTATAGTTAAA 1694
Db 301 ATGACTAATATTATGCTATAGTTAAA 326

RESULT 4

US-09-783-590-3523
; Sequence 3523, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Posen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: po-16 2c1
; CURRENT APPLICATION NUMBER: US/09/783,590
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3523
; LENGTH: 340
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (205)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (229)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (221)


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; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (895)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (886)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (907)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-800-729-23

Query Match
Best Local Similarity 100.0%; Score 80; DB 10; Length 922;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGACATCAGCGGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGCTGCAGG 60
      |||||||
Db 35 AGCTGACATCAGCGGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGCTGCAGG 94

QY 61 AATTCGGCAGCAGGAGG 80
      |||||||
Db 95 AATTCGGCAGCAGGAGG 114

RESULT 8
US-09-764-853-148
; Sequence 148, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 148
; LENGTH: 1772
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (1772)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-853-148

Query Match
Best Local Similarity 100.0%; Score 76; DB 10; Length 1772;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCGATTCAGCGGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGCTGCAGG 60
      |||||||
Db 42 AGTTCGATTCAGCGGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGCTGCAGG 101

QY 61 AATTCGGCAGCAGGAGG 75
      |||||||
Db 102 AATTCGGCAGCAGGAGG 117

RESULT 9
US-09-764-870-192/c
; Sequence 182, Application US/09764870
; Patent No. US20020042396A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P214
; CURRENT APPLICATION NUMBER: US/09/764,870
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 182
; LENGTH: 1355
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (44)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (55)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (126)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (132)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (164)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 182
; LENGTH: 1355
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (44)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (55)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (126)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (132)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (164)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE

Query Match
Best Local Similarity 100.0%; Score 75; DB 10; Length 1355;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGCTGCAGG 60
      |||||||
Db 911 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGCTGCAGG 852

QY 61 AATTCGGCAGCAGGAGG 75
      |||||||
Db 851 AATTCGGCAGCAGGAGG 837

RESULT 10
US-09-764-853-404/c
; Sequence 404, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 404
; LENGTH: 1355
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (44)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (55)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (126)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (132)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (164)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
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LOCATION: (1346)
OTHER INFORMATION: n equals a.t.g. or c
US-09-764-853-404

Query Match 4.2%; Score 75; DB 10; Length 1355;
Best Local Similarity 100.0%; Pred. No. 8.4e-29;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGGGTGGGGGGGGCTCTAGAACTAGTGGATGCGGGGGCTGGAAAG 40
|||||
DB 911 AGCTGGAGCTCCACCGGGTGGGGGGGGCTCTAGAACTAGTGGATGCGGGGGCTGGAAAG 40
|||||
QY 61 AATTCGGCAGGACC 75
|||||
DB 851 AATTCGGCAGGACC 837

RESULT 11

US-09-925-301-686
Sequence 586, Application US/09925301
Patent No US20020052308A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 686
LENGTH: 496
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (358)
OTHER INFORMATION: n equals a.t.g. or c
NAME/KEY: misc_feature
LOCATION: (417)
OTHER INFORMATION: n equals a.t.g. or c
NAME/KEY: misc_feature
LOCATION: (460)
OTHER INFORMATION: n equals a.t.g. or c
NAME/KEY: misc_feature
LOCATION: (472)
OTHER INFORMATION: n equals a.t.g. or c
NAME/KEY: misc_feature
LOCATION: (481)
OTHER INFORMATION: n equals a.t.g. or c
NAME/KEY: misc_feature
LOCATION: (488)
OTHER INFORMATION: n equals a.t.g. or c
US-09-925-301-686

Query Match 4.2%; Score 74; DB 10; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.6e-28;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGGGTGGGGGGGGCTCTAGAACTAGTGGATGCGGGGGCTGGAAAG 40
|||||
DB 18 AGCTGGAGCTCCACCGGGTGGGGGGGGCTCTAGAACTAGTGGATGCGGGGGCTGGAAAG 40
|||||
QY 61 AATTCGGCAGGACC 74
|||||
DB 78 AATTCGGCAGGACC 91

RESULT 12

US-09-908-711-28

Sequence 28, Application US/09908711
Patent No US20020045230A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA128
CURRENT APPLICATION NUMBER: US/09/908,711
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US01/01360
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,867
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US01/01344
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,892
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US01/01345
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,888
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US01/01329
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,905
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US01/01354
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,891
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US01/01339
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,869
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US01/01340
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,874
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US01/01334
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,898
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US01/01320
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,853
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US01/01349
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,902
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US01/01239
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,870
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US01/01348
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,882
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US01/01347
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,896
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US01/01307
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,864
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US01/01341
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,856
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US01/01336
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,868
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US01/01312

;; PRIOR FILING DATE: 2001-01-17
;; PRIOR APPLICATION NUMBER: 60/179,065
;; PRIOR FILING DATE: 2000-01-31
;; PRIOR APPLICATION NUMBER: 60/180,628
;; PRIOR FILING DATE: 2000-02-04
;; PRIOR APPLICATION NUMBER: 60/209,467
;; PRIOR FILING DATE: 2000-06-07
;; NUMBER OF SEQ ID NOS: 167
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 28
;; LENGTH: 640
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SITE
;; LOCATION: (555)
;; OTHER INFORMATION: n equals a,t,g, or c
;; NAME/KEY: SITE
;; LOCATION: (634)
;; OTHER INFORMATION: n equals a,t,g, or c
;; NAME/KEY: SITE
;; LOCATION: (638)
;; OTHER INFORMATION: n equals a,t,g, or c
US-09-908-711-28

Query Match 4.2%; Score 74; DB 10; Length 640;
Best Local Similarity 100.0%; Pred. No. 2.6e-28;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGCGCTGTGGCGCGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 60
|||||
DB 38 AGCTGGAGCTCCACCGCGCTGTGGCGCGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 97
|||||
QY 61 AATTCGGCAGCAGC 74
|||||
DB 98 AATTCGGCAGCAGC 111
|||||

RESULT 13
US-09-764-853-172
;; Sequence 172, Application US/09764853
;; Patent No. US20020090672A1
;; GENERAL INFORMATION:
;; APPLICANT: Rosen et al.
;; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;; FILE REFERENCE: PJ206
;; CURRENT APPLICATION NUMBER: US/09/764,853
;; CURRENT FILING DATE: 2001-01-17
;; Prior application data removed - consult PALM or file wrapper
;; NUMBER OF SEQ ID NOS: 939
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 172
;; LENGTH: 737
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SITE
;; LOCATION: (1)
;; OTHER INFORMATION: n equals a,t,g, or c
;; NAME/KEY: SITE
;; LOCATION: (4)
;; OTHER INFORMATION: n equals a,t,g, or c
;; NAME/KEY: SITE
;; LOCATION: (5)
;; OTHER INFORMATION: n equals a,t,g, or c
;; NAME/KEY: SITE
;; LOCATION: (6)
;; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-853-172

Query Match 4.2%; Score 74; DB 10; Length 737;
Best Local Similarity 100.0%; Pred. No. 2.7e-28;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGCGCTGTGGCGCGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 60
|||||
DB 48 AGCTGGAGCTCCACCGCGCTGTGGCGCGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 107
|||||
QY 61 AATTCGGCAGCAGC 74
|||||
DB 108 AATTCGGCAGCAGC 121
|||||

RESULT 14
US-09-764-853-305
;; Sequence 305, Application US/09764853
;; Patent No. US20020090672A1
;; GENERAL INFORMATION:
;; APPLICANT: Rosen et al.
;; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;; FILE REFERENCE: PJ206
;; CURRENT APPLICATION NUMBER: US/09/764,853
;; CURRENT FILING DATE: 2001-01-17
;; Prior application data removed - consult PALM or file wrapper
;; NUMBER OF SEQ ID NOS: 939
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 305
;; LENGTH: 791
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SITE
;; LOCATION: (694)
;; OTHER INFORMATION: n equals a,t,g, or c
;; NAME/KEY: SITE
;; LOCATION: (764)
;; OTHER INFORMATION: n equals a,t,g, or c
;; NAME/KEY: SITE
;; LOCATION: (778)
;; OTHER INFORMATION: n equals a,t,g, or c
;; NAME/KEY: SITE
;; LOCATION: (788)
;; OTHER INFORMATION: n equals a,t,g, or c
;; NAME/KEY: SITE
;; LOCATION: (789)
;; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-853-305

Query Match 4.2%; Score 74; DB 10; Length 791;
Best Local Similarity 100.0%; Pred. No. 2.7e-28;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGCGCTGTGGCGCGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 60
|||||
DB 40 AGCTGGAGCTCCACCGCGCTGTGGCGCGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 99
|||||
QY 61 AATTCGGCAGCAGC 74
|||||
DB 100 AATTCGGCAGCAGC 113
|||||

RESULT 15
US-09-764-853-365
;; Sequence 365, Application US/09764853
;; Patent No. US20020090672A1
;; GENERAL INFORMATION:
;; APPLICANT: Rosen et al.
;; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;; FILE REFERENCE: PJ206
;; CURRENT APPLICATION NUMBER: US/09/764,853
;; CURRENT FILING DATE: 2001-01-17
;; Prior application data removed - consult PALM or file wrapper
;; NUMBER OF SEQ ID NOS: 939
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 365
;; LENGTH: 796

DL 35 AGCTGAGCTTCACCGCGGCGGCTCTAGAACTAGTGGATCCCGGCTGACG 94
QY 61 AATTCGGCAGCAGC 74
Db 95 AATTCGGCAGCAGC 108

RESULT 19
US-09-764-864-91
; Sequence 91, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764.864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 91
; LENGTH: 1454
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-864-91

Query Match 4.2%, Score 74; DB 10; Length 1454;
Best Local Similarity 100.0%; Pred. No. 2.8e-28;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGCTTCACCGCGGCGGCTCTAGAACTAGTGGATCCCGGCTGACG 60
Db 10 AGCTGAGCTTCACCGCGGCTCTAGAACTAGTGGATCCCGGCTGACG 60
QY 61 AATTCGGCAGCAGC 74
Db 70 AATTCGGCAGCAGC 83

RESULT 20
US-09-764-870-217
; Sequence 217, Application US/09764870
; Patent No. US20020042386A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT214
; CURRENT APPLICATION NUMBER: US/09/764.870
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 217
; LENGTH: 1707
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1419)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-870-217

Query Match 4.2%, Score 74; DB 10; Length 1707;
Best Local Similarity 100.0%; Pred. No. 2.8e-28;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGCTTCACCGCGGCGGCTCTAGAACTAGTGGATCCCGGCTGACG 60
Db 39 AGCTGAGCTTCACCGCGGCGGCTCTAGAACTAGTGGATCCCGGCTGACG 98

QY 61 AATTCGGCAGCAGC 74
Db 99 AATTCGGCAGCAGC 112

RESULT 21
US-09-764-898-40
; Sequence 40, Application US/09764898
; Patent No. US20020090673A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ201
; CURRENT APPLICATION NUMBER: US/09/764.898
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 1788
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-898-40

Query Match 4.2%, Score 74; DB 10; Length 1788;
Best Local Similarity 100.0%; Pred. No. 2.8e-28;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGCTTCACCGCGGCTCTAGAACTAGTGGATCCCGGCTGACG 60
Db 31 AGCTGAGCTTCACCGCGGCTCTAGAACTAGTGGATCCCGGCTGACG 90
QY 61 AATTCGGCAGCAGC 74
Db 91 AATTCGGCAGCAGC 104

RESULT 22
US-09-764-903-22
; Sequence 22, Application US/09764903
; Patent No. US20020090674A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT228
; CURRENT APPLICATION NUMBER: US/09/764.903
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 2005
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (84)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (85)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (259)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1898)

; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1445)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1967)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-903-22

Query Match 4.2%; Score 74; DB 10; Length 2405;
Best Local Similarity 100.0%; Pred. No. 2 8e-28;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGCTCTACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGCTGCAGG 60
|||||
Db 330 AGCTGAGCTCTACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGCTGCAGG 389

QY 61 AATTCGGCAGCAGG 74
|||||
Db 390 AATTCGGCAGCAGG 403

RESULT 23

US-09-764-864-78
; Sequence 78, Application US/09764864
; Patent No. US20020132753A1

; GENERAL INFORMATION:
; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223

; CURRENT APPLICATION NUMBER: US/09/764,864
; Prior application data removed - consult PALM or file wrapper

; NUMBER OF SEQ ID NOS: 1792

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 78

; LENGTH: 2458

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (4)

; OTHER INFORMATION: n equals a,t,g, or c

; NAME/KEY: SITE

; LOCATION: (6)

; OTHER INFORMATION: n equals a,t,g, or c

; NAME/KEY: SITE

; LOCATION: (7)

; OTHER INFORMATION: n equals a,t,g, or c

; NAME/KEY: SITE

; LOCATION: (11)

; OTHER INFORMATION: n equals a,t,g, or c

US-09-764-864-78

Query Match 4.2%; Score 74; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 2 8e-28;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGCTCTACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGCTGCAGG 60
|||||
Db 50 AGCTGAGCTCTACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGCTGCAGG 109

QY 61 AATTCGGCAGCAGG 74
|||||
Db 110 AATTCGGCAGCAGG 123

RESULT 24

US-09-764-860-248/c

; Sequence 248, Application US/09764860

; Patent No. US20020094953A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC008
; CURRENT APPLICATION NUMBER: US/04/764,860
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1198
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 248
; LENGTH: 367
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

; NAME/KEY: SITE

; LOCATION: (345)

; OTHER INFORMATION: n equals a,t,g, or c

US-09-764-860-248

Query Match 4.1%; Score 73; DB 10; Length 367;
Best Local Similarity 100.0%; Pred. No. 8 4e-28;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGCTGCAGG 60
|||||
Db 334 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGCTGCAGG 275

QY 61 AATTCGGCAGCAGG 73
|||||
Db 274 AATTCGGCAGCAGG 262

RESULT 25

US-09-764-855-67

; Sequence 67, Application US/09764855

; Patent No. US20020119919A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: P110

; CURRENT APPLICATION NUMBER: US/09/764,855

; Prior application data removed - consult PALM or file wrapper

; NUMBER OF SEQ ID NOS: 334

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 67

; LENGTH: 421

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (1)

; OTHER INFORMATION: n equals a,t,g, or c

; NAME/KEY: SITE

; LOCATION: (6)

; OTHER INFORMATION: n equals a,t,g, or c

; NAME/KEY: SITE

; LOCATION: (12)

; OTHER INFORMATION: n equals a,t,g, or c

US-09-764-855-67

Query Match 4.1%; Score 73; DB 10; Length 421;
Best Local Similarity 100.0%; Pred. No. 8 5e-28;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGCTGCAGG 60
|||||
Db 28 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGCTGCAGG 87

QY 61 AATTCGGCAGCAGG 73
|||||
Db 88 AATTCGGCAGCAGG 100

RESULT 26

```
US-09-925-301-619
; Sequence 619, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PJ106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 619
; LENGTH: 604
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (371)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (440)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (492)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (500)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (537)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (554)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (584)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (587)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (593)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-301-619

Query Match 4.1%; Score 73; DB 10; Length 604;
Best Local Similarity 100.0%; Pred. No. 8.7e-28;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTTATCTGGGCTGGGCTCTAGAACTAGTGGATCCCGGGCTGCAGG 60
    |||||||
Db 28 AGCTGGAGCTTATCTGGGCTGGGCTCTAGAACTAGTGGATCCCGGGCTGCAGG 87

QY 61 AATTCGGCAGGAG 73
    |||||||
Db 88 AATTCGGCAGGAG 100

RESULT 27
US-09-764-853-136
; Sequence 136, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ206
```

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US-09-925-301-619
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 136
; LENGTH: 618
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (525)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (539)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (553)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-853-136

Query Match 4.1%; Score 73; DB 10; Length 618;
Best Local Similarity 100.0%; Pred. No. 8.7e-28;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTTCCACCGCGGTGGCGCGCTCTAGAACTAGTGGATCCCGGGCTGCAGG 60
    |||||||
Db 3 AGCTGGAGCTTCCACCGCGGTGGCGCGCTCTAGAACTAGTGGATCCCGGGCTGCAGG 62

QY 61 AATTCGGCAGGAG 73
    |||||||
Db 63 AATTCGGCAGGAG 75

RESULT 28
US-09-764-853-377
; Sequence 377, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 377
; LENGTH: 618
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (614)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (615)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (616)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-853-377

Query Match 4.1%; Score 73; DB 10; Length 618;
Best Local Similarity 100.0%; Pred. No. 8.7e-28;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTTCCACCGCGGTGGCGCGCTCTAGAACTAGTGGATCCCGGGCTGCAGG 60
    |||||||
Db 38 AGCTGGAGCTTCCACCGCGGTGGCGCGCTCTAGAACTAGTGGATCCCGGGCTGCAGG 97

QY 61 AATTCGGCAGGAG 73
    |||||||
```



```
Db 98 AATCGGCACGAG 110
RESULT 29
US-09-764-898-126
; Sequence 126, Application US/09764898
; Patent No. US2002090673A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P201
; CURRENT APPLICATION NUMBER: US/09/764 898
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 126
; LENGTH: 618
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (614)
; OTHER INFORMATION: n equals a.t.g. or c
; NAME/KEY: SITE
; LOCATION: (615)
; OTHER INFORMATION: n equals a.t.g. or c
; NAME/KEY: SITE
; LOCATION: (616)
; OTHER INFORMATION: n equals a.t.g. or c
US-09-764-898-126
Query Match 4.1%, Score 73; DB 10; Length 618;
Best Local Similarity 100.0%; Pred. No. 8.7e-28;
Matches 73, Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCTGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGCTGCAG 60
|||||
Db 38 AGCTGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGCTGCAG 97
|||||
QY 61 AATCGGCACGAG 73
|||||
Db 98 AATCGGCACGAG 110
RESULT 30
US-09-908-711-29
; Sequence 29, Application US/09908711
; Patent No. US20020045230A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P129
; CURRENT APPLICATION NUMBER: US/09/908,711
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US01/01360
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,867
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01344
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,892
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01345
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,888
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01329
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,905
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01354
; PRIOR FILING DATE: 2001-01-17
Query Match 4.1%, Score 73; DB 10; Length 631;
Best Local Similarity 100.0%; Pred. No. 8.7e-28;
Matches 73, Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGCTGCAG 60
|||||
Db 20 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGCTGCAG 79
|||||
; PRIOR APPLICATION NUMBER: 09/764,891
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01339
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,869
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01340
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,874
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01334
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,898
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01320
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,853
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01349
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,902
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01239
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,870
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01348
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,882
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01347
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,896
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01307
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,864
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01341
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,856
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01336
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,868
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01312
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 631
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (624)
; OTHER INFORMATION: n equals a.t.g. or c
US-09-908-711-29
Query Match 4.1%, Score 73; DB 10; Length 631;
Best Local Similarity 100.0%; Pred. No. 8.7e-28;
Matches 73, Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGCTGCAG 60
|||||
Db 20 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGCTGCAG 79
|||||
```

```
QY 61 AATTCGGCAGG 73
      |||||
Db 80 AATTCGGCAGG 92

RESULT 31
US-09-764-898-84
; Sequence 84, Application US/09764898
; Patent No. US2002009073A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P201
; CURRENT APPLICATION NUMBER: US/09/764,898
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (16)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (26)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (32)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (36)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (644)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (645)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (646)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (647)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-898-84

Query Match
Best Local Similarity 100.0%; Score 73; DB 10; Length 647;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTTCCACCGGTTGGTGTCTAGAACTAGTGGATCCCGGGCTGCAGG 60
      |||||
Db 42 AGCTGGAGCTTCCACCGGTTGGTGTCTAGAACTAGTGGATCCCGGGCTGCAGG 101

QY 61 AATTCGGCAGG 73
      |||||
Db 102 AATTCGGCAGG 114

RESULT 32
US-09-764-887-129
; Sequence 129, Application US/09764887
; Patent No. US20020042096A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PALL3
; CURRENT APPLICATION NUMBER: US/09/764,887
; CURRENT FILING DATE: 2001-01-17
```

```
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 658
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 129
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (558)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (607)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (722)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (758)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-887-129

Query Match
Best Local Similarity 100.0%; Score 73; DB 10; Length 771;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTTCCACCGGTTGGTGTCTAGAACTAGTGGATCCCGGGCTGCAGG 60
      |||||
Lb 16 AGCTGGAGCTTCCACCGGTTGGTGTCTAGAACTAGTGGATCCCGGGCTGCAGG 75

QY 61 AATTCGGCAGG 73
      |||||
Db 76 AATTCGGCAGG 88

RESULT 33
US-09-764-864-289
; Sequence 289, Application US/09764864
; Patent No. US20020132759A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 289
; LENGTH: 869
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (806)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (833)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (865)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-864-289

Query Match
Best Local Similarity 100.0%; Score 73; DB 10; Length 869;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTTCCACCGGTTGGTGTCTAGAACTAGTGGATCCCGGGCTGCAGG 60
      |||||
Db 3 AGCTGGAGCTTCCACCGGTTGGTGTCTAGAACTAGTGGATCCCGGGCTGCAGG 62

QY 61 AATTCGGCAGG 73
```

```
Db 63 AATTGGGACGAG 75
|||||
RESULT 34
US-09-789-561-58
; Sequence 58, Application US/09789561
; Patent No. US20020064818A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 52 Human secreted proteins
; CURRENT APPLICATION NUMBER: US/09/789,561
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: PCT/US00/24008
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/152,317
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/152,315
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
; LENGTH: 975
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-789-561-58

Query Match 4.1%; Score 73; DB 10; Length 975;
Best Local Similarity 100.0%; Pred. No. 8.9e-28;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGGGTGGCGGCTCTAGAACTAGTATGATCCCGGCTGCAGG 60
Db 20 AGCTGGAGCTCCACCGGGTGGCGGCTCTAGAACTAGTATGATCCCGGCTGCAGG 60
|||||
QY 61 AATTGGGACGAG 73
Db 80 AATTGGGACGAG 92
|||||

RESULT 35
US-09-764-898-54
; Sequence 54, Application US/09764898
; Patent No. US20020090673A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P201
; CURRENT APPLICATION NUMBER: US/09/764,898
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 1066
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: n equals a.t.g, or c
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: n equals a.t.g, or c
US-09-764-898-54

Query Match 4.1%; Score 73; DB 10; Length 1066;
Best Local Similarity 100.0%; Pred. No. 8.9e-28;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGGGTGGCGGCTCTAGAACTAGTATGATCCCGGCTGCAGG 60
Db 1 AGCTGGAGCTCCACCGGGTGGCGGCTCTAGAACTAGTATGATCCCGGCTGCAGG 60
|||||
QY 61 AATTGGGACGAG 73
Db 54 AATTGGGACGAG 106
|||||

RESULT 36
US-09-925-300-639
; Sequence 639, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 639
; LENGTH: 1427
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (6)
; OTHER INFORMATION: n equals a.t.g, or c
; NAME/KEY: misc feature
; LOCATION: (9)
; OTHER INFORMATION: n equals a.t.g, or c
; NAME/KEY: misc feature
; LOCATION: (12)
; OTHER INFORMATION: n equals a.t.g, or c
; NAME/KEY: misc feature
; LOCATION: (29)
; OTHER INFORMATION: n equals a.t.g, or c
US-09-925-300-639

Query Match 4.1%; Score 73; DB 10; Length 1427;
Best Local Similarity 100.0%; Pred. No. 9e-28;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGGGTGGCGGCTCTAGAACTAGTATGATCCCGGCTGCAGG 60
Db 34 AGCTGGAGCTCCACCGGGTGGCGGCTCTAGAACTAGTATGATCCCGGCTGCAGG 60
|||||
QY 61 AATTGGGACGAG 73
Db 54 AATTGGGACGAG 106
|||||

RESULT 37
US-09-764-853-308/c
; Sequence 308, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 308
; LENGTH: 1511
; TYPE: DNA
; ORGANISM: Homo sapiens
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; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1511)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-853-308

Query Match
Best Local Similarity 100.0%; Score 73; DB 10; Length 1511;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGCGGTGGCGGCGGCTCTAGAACTAGTGGATCCCGGGGCTGCAGG 60
Db 1205 AGCTGGAGCTCCACCGCGGTGGCGGCGGCTCTAGAACTAGTGGATCCCGGGGCTGCAGG 60
QY 61 AATTCGGCAGCAG 73
Db 1145 AATTCGGCAGCAG 1133

RESULT 38
US-09-739-254-64
; Sequence 64, Application US/09739254
; Patent No. US20010021700A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 49 Human Secreted Proteins
; FILE REFERENCE: P2032P1
; CURRENT APPLICATION NUMBER: US/09/739,254
; CURRENT FILING DATE: 2000-12-19
; EARLIER APPLICATION NUMBER: 09/511,554
; EARLIER FILING DATE: 2000-02-23
; EARLIER APPLICATION NUMBER: PCT/US99/19350
; EARLIER FILING DATE: 1999-08-24
; EARLIER APPLICATION NUMBER: 60/097,917
; EARLIER FILING DATE: 1998-08-25
; EARLIER APPLICATION NUMBER: 60/098,634
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-739-254-64

Query Match
Best Local Similarity 100.0%; Score 73; DB 10; Length 1517;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGCGGTGGCGGCGGCTCTAGAACTAGTGGATCCCGGGGCTGCAGG 60
Db 1205 AGCTGGAGCTCCACCGCGGTGGCGGCGGCTCTAGAACTAGTGGATCCCGGGGCTGCAGG 60
QY 61 AATTCGGCAGCAG 73
Db 1145 AATTCGGCAGCAG 1133

RESULT 39
US-09-904-615-64
; Sequence 64, Application US/09904615
; Patent No. US20020226040A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 49 Human Secreted Proteins
; FILE REFERENCE: P2032P1
; CURRENT APPLICATION NUMBER: US/09/904,615
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/511,554
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/097,917
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: 60/098,634
; PRIOR FILING DATE: 1998-08-31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-904-615-64

Query Match
Best Local Similarity 100.0%; Score 73; DB 10; Length 1517;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGCGGTGGCGGCGGCTCTAGAACTAGTGGATCCCGGGGCTGCAGG 60
Db 1205 AGCTGGAGCTCCACCGCGGTGGCGGCGGCTCTAGAACTAGTGGATCCCGGGGCTGCAGG 60
QY 61 AATTCGGCAGCAG 73
Db 1145 AATTCGGCAGCAG 1133

RESULT 40
US-09-874-923-54
; Sequence 54, Application US/09874923
; Patent No. US20020081320A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, David C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Bhatia, Ajay
; APPLICANT: Coler, Rhea
; APPLICANT: Probst, Peter
; APPLICANT: Brannon, Mark
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; THERAPY AND DIAGNOSIS OF LEISHMANIASIS
; FILE REFERENCE: 210121.420C8
; CURRENT APPLICATION NUMBER: US/09/874,923
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 1585
; TYPE: DNA
; ORGANISM: Leishmania major
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1).....(1585)
; OTHER INFORMATION: n = A,T,C or G
US-09-874-923-54

Query Match
Best Local Similarity 100.0%; Score 73; DB 10; Length 1585;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGCGGTGGCGGCGGCTCTAGAACTAGTGGATCCCGGGGCTGCAGG 60
Db 3 AGCTGGAGCTCCACCGCGGTGGCGGCGGCTCTAGAACTAGTGGATCCCGGGGCTGCAGG 62
QY 61 AATTCGGCAGCAG 73
Db 63 AATTCGGCAGCAG 75

RESULT 41
US-09-925-300-770
; Sequence 770, Application US/99925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben

```

; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 770
; LENGTH: 1637
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-300-770

Query Match 4.1%; Score 73; DB 10; Length 1637;
Best Local Similarity 100.0%; Pred. No. 9.1e-28;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCTGGAGCTCCACCGCGGTGGCGGCTCTATGAATTAAGTGGATCCCGGGGCTGCAGG 60
|||||
Db 4 AGCTGGAGCTCCACCGCGGTGGCGGCTCTATGAATTAAGTGGATCCCGGGGCTGCAGG 60
QY 61 AATTCGGCAGGAG 73
|||||
Db 64 AATTCGGCAGGAG 76

RESULT 42

US-09-862-027-13
; Sequence 13, Application US/09862027
; Patent No. US20020142428A1
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; TITLE OF INVENTION: No. US20020142428A1 Kinases and Uses Thereof
; FILE REFERENCE: 35800/234862
; CURRENT APPLICATION NUMBER: US/09/862,027
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 09/345,473
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 1737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (275)....(1522)
US-09-862-027-13

Query Match 4.1%; Score 73; DB 10; Length 1737;
Best Local Similarity 100.0%; Pred. No. 9.1e-28;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCTGGAGCTCCACCGCGGTGGCGGCTCTATGAATTAAGTGGATCCCGGGGCTGCAGG 60
|||||
Db 2 AGCTGGAGCTCCACCGCGGTGGCGGCTCTATGAATTAAGTGGATCCCGGGGCTGCAGG 60
QY 61 AATTCGGCAGGAG 73
|||||
Db 81 AATTCGGCAGGAG 93

RESULT 43

US-09-739-254-32
; Sequence 32, Application US/09739254
; Patent No. US20010021700A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 49 Human Secreted Proteins
; FILE REFERENCE: P2032P1

; CURRENT APPLICATION NUMBER: US/09/739,254
; CURRENT FILING DATE: 2000-12-19
; EARLIER APPLICATION NUMBER: 09/511,554
; EARLIER FILING DATE: 2000-02-23
; EARLIER APPLICATION NUMBER: PCT/US99/19330
; EARLIER FILING DATE: 1999-08-24
; EARLIER APPLICATION NUMBER: 60/097,917
; EARLIER FILING DATE: 1998-08-25
; EARLIER APPLICATION NUMBER: 60/098,634
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 1906
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (617)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (940)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1461)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1901)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-739-254-32

Query Match 4.1%; Score 73; DB 10; Length 1906;
Best Local Similarity 100.0%; Pred. No. 9.2e-28;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CTGAGCTCCACCGCGGTGGCGGCTCTATGAATTAAGTGGATCCCGGGGCTGCAGGAA 62
|||||
Db 2 CTGAGCTCCACCGCGGTGGCGGCTCTATGAATTAAGTGGATCCCGGGGCTGCAGGAA 61
QY 63 TTGGGCAGGAGCC 75
|||||
Db 62 TTGGGCAGGAGCC 74

RESULT 44

US-09-904-615-32
; Sequence 32, Application US/09904615
; Patent No. US20020026040A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 49 Human Secreted Proteins
; FILE REFERENCE: P2032P1
; CURRENT APPLICATION NUMBER: US/09/904,615
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/511,554
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/097,917
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: 60/098,634
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 1906
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (617)
; OTHER INFORMATION: n equals a,t,g, or c

```
; NAME/KEY: SITE
; LOCATION: (940)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1461)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1901)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-904-615-32

Query Match
Best Local Similarity 4.1%; Score 73; DB 10; Length 1906;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CTGAGAGTCACCGCGGTGGCGCGCTCTAGAACTAGTGGTATGCGCGCGGTTCGACGAA 62
Db 2 CTGAGATTCACCGCGGTGGCGCGCTCTAGAACTAGTGGTATGCGCGCGGTTCGACGAA 61
QY 63 TTCGGCAGCAGCC 75
Db 62 TTCGGCAGCAGCC 74

RESULT 45
US-09-789-561-53
; Sequence 53, Application US/09789561
; Patent No. US20020064818A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; FILE REFERENCE: P2043P1
; CURRENT APPLICATION NUMBER: US/09/789,561
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: PCT/US00/24008
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/152,317
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/152,315
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53
; LENGTH: 2163
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (15)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-789-561-53

Query Match
Best Local Similarity 4.1%; Score 73; DB 10; Length 2163;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGCGGTGGCGCGCTCTAGAACTAGTGGTATGCGCGCGGTTCGACGAA 60
Db 48 AGCTGGAGCTCCACCGCGGTGGCGCGCTCTAGAACTAGTGGTATGCGCGCGGTTCGACGAA 60
QY 61 AATTCGGCAGCAG 73
Db 108 AATTCGGCAGCAG 120

RESULT 46
US-09-764-870-222/c
; Sequence 221, Application US/09764870
; Patent No. US2002004286A1
; GENERAL INFORMATION:
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; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT214
; CURRENT APPLICATION NUMBER: US/09/764,870
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 222
; LENGTH: 2244
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (10)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (11)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (2007)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (2121)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-870-222

Query Match
Best Local Similarity 4.1%; Score 73; DB 10; Length 2244;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGCGGTGGCGCGCTCTAGAACTAGTGGTATGCGCGCGGTTCGACGAG 60
Db 1766 AGCTGGAGCTCCACCGCGGTGGCGCGCTCTAGAACTAGTGGTATGCGCGCGGTTCGACGAG 1707
QY 61 AATTCGGCAGCAG 73
Db 1706 AATTCGGCAGCAG 1694

RESULT 47
US-09-764-853-189
; Sequence 189, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 189
; LENGTH: 2330
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
US-09-764-853-189

Query Match
Best Local Similarity 4.1%; Score 73; DB 10; Length 2330;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGCGGTGGCGCGCTCTAGAACTAGTGGTATGCGCGCGGTTCGACGAG 60
Db 38 AGCTGGAGCTCCACCGCGGTGGCGCGCTCTAGAACTAGTGGTATGCGCGCGGTTCGACGAG 97
QY 61 AATTCGGCAGCAG 73
Db 98 AATTCGGCAGCAG 110

RESULT 48
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US-09-764-853-380
; Sequence 380, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 380
; LENGTH: 2596
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: n equals a.t.g, or c
; NAME/KEY: SITE
; LOCATION: (2508)
; OTHER INFORMATION: n equals a.t.g, or c
; NAME/KEY: SITE
; LOCATION: (2529)
; OTHER INFORMATION: n equals a.t.g, or c
; NAME/KEY: SITE
; LOCATION: (2556)
; OTHER INFORMATION: n equals a.t.g, or c
US-09-764-853-380

Query Match 4.1%, Score 73; DB 10; Length 2596;
Best Local Similarity 100.0%; Pred. No. 9.3e-28;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCTGGAGCTCCACCGCGGTGGCGGCGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 60
Db 33 AGCTGGAGCTCCACCGCGGTGGCGGCGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 92
QY 61 AATTCGGCAGGAG 73
Db 93 AATTCGGCAGGAG 105

RESULT 49
US-09-764-898-128
; Sequence 128, Application US/09764898
; Patent No. US20020090673A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P201
; CURRENT APPLICATION NUMBER: US/09/764,898
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 128
; LENGTH: 2596
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: n equals a.t.g, or c
; NAME/KEY: SITE
; LOCATION: (2508)
; OTHER INFORMATION: n equals a.t.g, or c
; NAME/KEY: SITE
; LOCATION: (2529)
; OTHER INFORMATION: n equals a.t.g, or c
; NAME/KEY: SITE
; LOCATION: (2556)

; OTHER INFORMATION: n equals a.t.g, or c
US-09-764-898-128

Query Match 4.1%, Score 73; DB 10; Length 2596;
Best Local Similarity 100.0%; Pred. No. 9.3e-28;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCTGGAGCTCCACCGCGGTGGCGGCGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 60
Db 33 AGCTGGAGCTCCACCGCGGTGGCGGCGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 92
QY 61 AATTCGGCAGGAG 73
Db 93 AATTCGGCAGGAG 105

RESULT 50
US-09-789-561-64
; Sequence 64, Application US/09789561
; Patent No. US20020064818A1
; GENERAL INFORMATION:
; APPLICANT: N1 et al.
; TITLE OF INVENTION: 52 Human secreted proteins
; FILE REFERENCE: P2043P1
; CURRENT APPLICATION NUMBER: US/09/789,561
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: PCT/US00/24008
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/152,317
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/152,315
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 2751
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-789-561-64

Query Match 4.1%, Score 73; DB 10; Length 2751;
Best Local Similarity 100.0%; Pred. No. 9.4e-28;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCTGGAGCTCCACCGCGGTGGCGGCGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 60
Db 24 AGCTGGAGCTCCACCGCGGTGGCGGCGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 83
QY 61 AATTCGGCAGGAG 73
Db 84 AATTCGGCAGGAG 96

Search completed: October 31, 2002, 12:44:30
Job time : 80 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 31, 2002, 10:10:50 : Search time 64 Seconds
(without alignments)
8500 696 Million cell updates/sec

Title: US-09-854-300-7

Perfect score: 1774

Sequence: 1 agctggagctccaccggcgtt..... atagggaagtcttctctctcag 1774

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database : Issued_Patents_NA.*

- 1: /cgn2_6/ptodata/1/ina/5A.COMR.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B.COMR.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PTUS.COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	77	4.3	912	2	US-09-090-567-3
2	74	4.2	2605	2	US-08-680-395-4
3	73	4.1	545	4	US-09-227-357-125
4	73	4.1	1378	1	US-08-075-533-20
5	73	4.1	1378	2	US-08-948-176-20
6	73	4.1	1378	5	PCT-US91-09160-20
7	73	4.1	1556	4	US-09-043-937A-3
8	73	4.1	1568	4	US-09-043-937A-1
9	73	4.1	1585	4	US-09-183-861-54
10	73	4.1	1585	4	US-09-022-765-54
11	73	4.1	2775	1	US-08-730-771-1
12	73	4.1	2775	4	US-09-060-208-1
13	73	4.1	3089	1	US-08-472-934-5
14	73	4.1	3089	2	US-08-323-460A-5
15	73	4.1	3089	2	US-08-461-146C-5
16	73	4.1	3089	3	US-08-461-145C-5
17	73	4.1	3089	4	US-08-638-823-3
18	73	4.1	3328	4	US-08-960-048-1
19	73	4.0	2045	4	US-08-795-088A-1
20	70	3.9	2085	2	US-08-668-128E-7
21	70	3.9	2085	2	US-08-905-445-7
22	67	3.8	500	4	US-08-818-112-101
23	67	3.8	500	4	US-08-818-111-96
24	67	3.8	500	4	US-09-056-556-101
25	67	3.8	500	4	US-09-072-596-96
26	66	3.7	752	4	US-08-976-259-108
27	66	3.7	849	3	US-08-646-538-14

28	66	3.7	849	4	US-09-503-222-14	Sequence 14, Appl
29	66	3.7	1924	4	US-09-424-283-5	Sequence 5, Appl
30	66	3.7	1958	4	US-09-215-221-9	Sequence 9, Appl
31	66	3.7	2961	4	US-08-446-935-6	Sequence 6, Appl
32	66	3.7	3699	3	US-08-646-538-6	Sequence 6, Appl
33	66	3.7	3699	4	US-09-503-222-6	Sequence 6, Appl
34	66	3.7	3792	2	US-08-992-334-1	Sequence 1, Appl
35	66	3.7	3792	3	US-08-302-752-1	Sequence 2, Appl
36	66	3.7	5234	2	US-08-992-334-2	Sequence 1, Appl
37	66	3.7	5234	3	US-08-302-752-3	Sequence 2, Appl
38	66	3.7	6045	3	US-08-675-566-18	Sequence 18, Appl
39	66	3.7	6244	3	US-08-675-566-17	Sequence 17, Appl
40	66	3.7	6447	3	US-08-675-566-16	Sequence 16, Appl
41	66	3.7	6578	3	US-08-675-566-14	Sequence 4, Appl
42	66	3.7	6612	3	US-08-675-566-15	Sequence 15, Appl
43	66	3.7	6722	3	US-08-992-334-3	Sequence 3, Appl
44	66	3.7	6722	3	US-08-302-752-3	Sequence 2, Appl
45	66	3.7	6958	3	US-08-675-566-2	Sequence 2, Appl
46	66	3.7	6994	3	US-08-675-566-1	Sequence 1, Appl
47	66	3.7	7001	3	US-08-675-566-3	Sequence 3, Appl
48	66	3.7	7287	2	US-08-659-206A-1	Sequence 1, Appl
49	65	3.7	1058	4	US-08-818-112-14	Sequence 14, Appl
50	65	3.7	1058	4	US-08-818-111-14	Sequence 14, Appl
51	65	3.7	1058	4	US-09-056-556-14	Sequence 14, Appl
52	65	3.7	1058	4	US-09-072-596-14	Sequence 14, Appl
53	65	3.7	1830	1	US-08-343-733A-2	Sequence 2, Appl
54	65	3.7	2082	4	US-09-233-505-9	Sequence 9, Appl
55	65	3.7	3023	4	US-09-308-022-4	Sequence 4, Appl
56	63	3.6	229	4	US-09-116-492A-39	Sequence 39, Appl
57	63	3.6	278	2	US-08-713-000-10	Sequence 10, Appl
58	63	3.6	278	2	US-08-975-316-10	Sequence 10, Appl
59	63	3.6	278	4	US-09-211-710-10	Sequence 10, Appl
60	63	3.6	278	4	US-09-615-192A-10	Sequence 10, Appl
61	63	3.6	300	1	US-08-644-664B-24	Sequence 24, Appl
62	63	3.6	300	2	US-08-761-277A-24	Sequence 24, Appl
63	63	3.6	803	2	US-08-967-101-117	Sequence 117, App
64	63	3.6	803	2	US-08-592-541-117	Sequence 117, App
65	63	3.6	803	3	US-09-124-698-117	Sequence 117, App
66	63	3.6	803	4	US-09-127-480-117	Sequence 117, App
67	63	3.6	803	4	US-08-496-841C-117	Sequence 117, App
68	63	3.6	803	4	US-09-124-523-117	Sequence 117, App
69	63	3.6	1264	1	US-08-006-082A-1	Sequence 1, Appl
70	63	3.6	2842	2	US-08-175-388-3	Sequence 3, Appl
71	63	3.6	2842	2	US-08-779-620-3	Sequence 3, Appl
72	63	3.6	2842	2	US-08-818-726-3	Sequence 3, Appl
73	63	3.6	3198	4	US-08-842-306B-48	Sequence 48, Appl
74	63	3.6	3198	4	US-08-838-973B-48	Sequence 48, Appl
75	62	3.5	1053	4	US-09-183-861-48	Sequence 48, Appl

ALIGNMENTS

RESULT 1
US-09-090-567-3
; Sequence 3, Application US/09090567
; Patent No. 5989549
; GENERAL INFORMATION:
; APPLICANT: Sullivan, Robert
; APPLICANT: Brub, Bruno
; APPLICANT: Lgar, Christine
; APPLICANT: Gaudreault, Christian
; TITLE OF INVENTION: Acrosomal Sperm Protein And
; TITLE OF INVENTION: Uses Thereof
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swabey Ogilvy Renault
; STREET: 1600 - 1381 McGill College
; CITY: Montreal
; STATE: QC
; COUNTRY: Canada
; ZIP: H3A 2Y3
; COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/090,567
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Murphy, Kevin P
REGISTRATION NUMBER: 26,674
REFERENCE/DOCKET NUMBER: 13045-2"US" FC/CC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 514-845-7126
TELEFAX: 514-288-8389
TELEX:
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS
LENGTH: 912 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
US-09-090-567-3

Query Match 4.3%; Score 77; DB 2; Length 912;
Best Local Similarity 100.0%; Pred. No. 5e-29;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGACTCTACCGGCGGCGGCGCTGTAGAACTATATGATCCCGCGGCTGCAAG 60
Db 7 AGCTGAGACTCTACCGGCGGCGGCGGCGCTGTAGAACTATATGATCCCGCGGCTGCAAG 60

QY 61 AATTCGGCAGCAGCGCA 77
Db 67 AATTCGGCAGCAGCGCA 83

RESULT 2
US-08-680-395-4
Sequence 4, Application US/08680395
Patent No. 5892010
GENERAL INFORMATION:
APPLICANT: Gray, Joe W
APPLICANT: Collins, Colin
APPLICANT: Hwang, Soc-in
APPLICANT: Godfrey, Tony
APPLICANT: Kowbel, David
APPLICANT: Rommens, Johanna
TITLE OF INVENTION: Genes from the 20q13 Amplicon and Their
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3634
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.70
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/680,395
FILING DATE: 15-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 024070-06890005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ. ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2605 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: -
LOCATION: 1,2605
OTHER INFORMATION: (note="cDNA clone ccd3 of 4 kb
OTHER INFORMATION: transcript")
US-08-680-395-4

Query Match 4.3%; Score 74; DB 2; Length 2605;
Best Local Similarity 100.0%; Pred. No. 1.6e-27;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGACTCTACCGGCGGCGGCGCTGTAGAACTATATGATCCCGCGGCTGCAAG 60
Db 36 AGCTGAGACTCTACCGGCGGCGGCGGCGCTGTAGAACTATATGATCCCGCGGCTGCAAG 95

QY 61 AATTCGGCAGCAGC 74
Db 96 AATTCGGCAGCAGC 109

RESULT 3
US-09-227-357-125
Sequence 125, Application US/99227357
Patent No. 6342581
GENERAL INFORMATION:
APPLICANT: Fischer et al.
TITLE OF INVENTION: 123 Human Secreted Proteins
FILE REFERENCE: P2010P1
CURRENT APPLICATION NUMBER: US/09/227,357
EARLIER FILING DATE: 1999-01-08
EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: 60/051,926
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,793
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,925
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,929
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,803
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,732
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,931
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,932
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,916
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,930
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,918
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,920
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,733
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,795
EARLIER FILING DATE: 1997-07-08

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; EARLIER APPLICATION NUMBER: 60/051,919
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,928
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/055,722
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,723
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,948
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,949
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,953
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,950
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,947
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,964
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/056,360
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,684
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,984
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,954
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/058,785
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,564
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,660
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,661
; EARLIER FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 672
; SEQ ID NO 125
; SOFTWARE: PatentIn Ver. 2.0
; LENGTH: 545
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (7)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (16)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (41)
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; FEATURE:
; NAME/KEY: SITE
; LOCATION: (42)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (87)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-227-357-125

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Query Match      4.1%; Score 73; DB 4; Length 545;
Best Local Similarity 100.0%; Pred. No. 5.1e-27;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCTGGAGCTCCACGGGTGGCGGCTCTAGAACTAGTGGATCCCGGGCTGCAGG 60
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Db 117 ACCTGGAGCTCCACGGGTGGCGGCTCTAGAACTAGTGGATCCCGGGCTGCAGG 176
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QY 61 AATTGGCAGCAG 73

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RESULT 5
US-08-948-176-20
; Sequence 20, Application US/08948176
; Patent No. 5945585
; GENERAL INFORMATION:
; APPLICANT: HITZ, WILLIAM D.
; APPLICANT: YADAV, NARENDRA S.
; TITLE OF INVENTION: ACYL-ACP THIOESTERASES GENES

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Db 177 AATTGGCAGCAG 189
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RESULT 4

```

US-08-075-533-20
; Sequence 20, Application US/08075533
; Patent No. 5530186
; GENERAL INFORMATION:
; APPLICANT: Hitz, William D.
; APPLICANT: Yadav, Narendra S.
; TITLE OF INVENTION: Nucleotide Sequences of Soybean Acyl-ACP
; TITLE OF INVENTION: Thioesterase Genes
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,533
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/631,264
; FILING DATE: 20-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Morrissey, Bruce W.
; REGISTRATION NUMBER: 30,663
; REFERENCE/DOCKET NUMBER: CP-8926-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4927
; TELEFAX: (302) 892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1378 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Brassica napus
US-08-075-533-20

```

```

Query Match      4.1%; Score 73; DB 1; Length 1378;
Best Local Similarity 100.0%; Pred. No. 5.1e-27;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AATTGGAGCTCCACGGGTGGCGGCTCTAGAACTAGTGGATCCCGGGCTGCAGG 60
   |||||||
Db 52 ACCTGGAGCTCCACGGGTGGCGGCTCTAGAACTAGTGGATCCCGGGCTGCAGG 111
   |||||||

QY 61 AATTGGCAGCAG 73
   |||||||
Db 112 AATTGGCAGCAG 124

```

```

RESULT 5
US-08-948-176-20
; Sequence 20, Application US/08948176
; Patent No. 5945585
; GENERAL INFORMATION:
; APPLICANT: HITZ, WILLIAM D.
; APPLICANT: YADAV, NARENDRA S.
; TITLE OF INVENTION: ACYL-ACP THIOESTERASES GENES

```

```

Query Match Similarity      4.1%; Score 73; DB 2; Length 1378;
Best Local Similarity      100.0%; Pred. No. 5, le-27;
Matches       73; Conservative    0; Mismatches     0; Indels     0; Gaps     0;

OY          1 AGCTGGAGCCTCCACCGGCGTGGCGCGGTCTATGAACAATTATGTGCAATCTCATTTGAGTAAAGGAGG
              |||
DB           52 AGCTGGAGCTCCACCGGCGTGGCGGCGGTCTATGAACAATAATGTGCAATCTCATTTGAGTAAAGG 111
OY          61 ATTCTGGCACGAG 73
              |||
DB          112 AATTGGGCACGAG 124

RESULT 6
PCT-US91-09160-20
Sequence 20 Application FC/TUSUJ09160
GENERAL INFORMATION.
APPLICANT: Hitz, William D.
APPLICANT: Yadav, Narendra S.
TITLE OF INVENTION: Nucleotide Sequences of Soybean Acyl-ACP
TITLE OF INVENTION: Thioesterase Genes
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: U.S.A
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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```

Query Match 4.1% Score 73 DB 5; Length 1378;
Best Local Similarity 100.0% Pred. 5.1e-27;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

C: 1 ACGTGGAGCTCCACCGCGGCGGCGGCTTTAGAAATAGTGGATCCCGCGGCTGACG 66
Db 52 ACGTGGAGCTCCACCGCGGCGGCGGCTTTAGAAATAGTGGATCCCGCGGCTGACG 111

C: 61 AATTGGGACACGAG 73
Db 112 AATTGGGACACGAG 124

```

RESULT 7
 US-09-043-937A-3
 ; Sequence 3, Application US/09043937A
 ; Patent No. 6211432
 ; GENERAL INFORMATION:
 APPLICANT: BOUDET, ALAIN-MICHEL
 PICHON, MAGALIE
 GRIMA-PETENATI, JACQUELINE
 BECKERT, MICHEL
 GAMAS, PASCAL
 BRIAT, JEAN-FRANCOIS
 TITLE OF INVENTION: DNA SEQUENCES CODING FOR CINNAMOYL-CoA
 REDUCTASE, AND APPLICATIONS THEREOF IN THE CONTROL OF
 LIGNIN CONTENTS IN PLANTS
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHYE, P C
 STREET: 110 NORTH GLEBE ROAD, 8TH FLOOR
 CITY: ARLINGTON
 STATE: VA
 COUNTRY: USA
 ZIP: 22201
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/043,937A
 FILING DATE: 24-Jul-1998
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION NUMBER: WO PCT/FR96/01544

FILING DATE: 03-OCT-1996
 APPLICATION NUMBER: FR 95.11623
 FILING DATE: 03-OCT-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: SADOFF, B.J.
 REGISTRATION NUMBER: 36.663
 REFERENCE/DOCKET NUMBER: 1497-20
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-816-4000
 TELEFAX: 703-816-4100
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1556 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 195 1310
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 UG-09-043-937A-3

```

Query Match      4.18; Score 73; DB 4; Length 1556.
Best Local Similarity 100.0%; Pred. No. 5.le-27;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 AGCTGAGTCTACCGCGGTGCGCGCGCTCTAGAACTATGTGATCTGCGCGGTGCGCG 60
    |||||
DL 52 AGTGGAGCTGACGGGTGCGCGGTGCGCGGTCTAGAACTATGTGATCTGCGCGGTGCGCG 111
    |||||

QY 61 AATTGCGCACGAG 73
    |||||
Db 112 AATTGCGCACGAG 124

```

RESULT 8
US-09-043-937A-1
; Sequence 1, Application US/09043937A
; Patent No. 6211432
; GENERAL INFORMATION:

```

: APPLICANT: BOUDET, ALAIN-MICHEL
: PICHON, MAGALIE
: GRIMA-PETTENATI, JACQUELINE
: BECKERT, MICHEL
: GAMAIS, PASCAL
: BRIAT, JEAN-FRANCOIS
: TITLE OF INVENTION: DNA SEQUENCES CODING FOR THE PRODUCTION OF A REDUCTASE, AND APPLICATIONS TO THE ANALYSIS OF LIGNIN CONTENTS IN WOODS

```

NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE, P.C.
STREET: 110 NORTH GLERE ROAD, 8TH FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/043,937A
FILING DATE: 24-Jul-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FP96/01544
FILING DATE: 03-OCT-1996
APPLICATION NUMBER: FP 95,11623
FILING DATE: 03-OCT-1995
ATTORNEY/AGENT INFORMATION:

```

? NAME: SADOFF, B.J.
? REGISTRATION NUMBER: 36.663
? REFERENCE/DONOR FFT NUMRFP: 1487-20
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 703-816-4000
? TELEFAX: 703-816-4100
? INFORMATION FOR SEQ ID NO. 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1568 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA to mRNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 278..1306
? SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-043-937A-1

Query Match          4.1%, Score 73, DB 4; Length 1568;
Best Local Similarity 100.0%; Pred.No. 5.1e-27;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCTGGAGTTCACCGGCGGTGGGCGGCGGTTATGAACATATGATGCCCGGCGGCGCAAG 50
      |||.....
Db   47 ACGTGAGCACCACGGCGGTGGGCGGCGGTTATGAACATATGATGCCCGGCGGCGCAAG 106
      |||.....

QY 61 AATTGGGCACGAG 73
      |||.....
Db 107 AATTGGGCACGAG 119

```

RESULT 9
US-09-183-861-54
; Sequence 54, Application US/09183861

Patent No. 6365165

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Campos Neto, Antonio

APPLICANT: Webb, John R.

APPLICANT: Dillon, Devin C.

APPLICANT: Skeiky, Yasir A.W.

TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE THERAPY AND

NUMBER OF SEQUENCES: 87

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED AND BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/183,861

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/022,765

FILING DATE: 12-FEB-1998

ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/POCKET NUMBER: 21021.420C3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 54.

SEQUENCE CHARACTERISTICS:

LENGTH: 1585 base pairs


```

: NUMBER OF SEQUENCES: 1
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Ratner & Prestia
: STREET: P.O. Box 980
: CITY: Valley Forge
: STATE: PA
: COUNTRY: USA
: ZIP: 19482-0980
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq Version 1.5
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US-00-060-208
: FILING DATE: April 15, 1998
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Prestia, Paul F.
: REGISTRATION NUMBER: 23,031
: REFERENCE/POCKET NUMBER: P50380-1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 610-407-0700
: TELEFAX: 610-407-0701
: TELEX: 846169
: INFORMATION F# SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2775 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: FRAGMENT TYPE:
: ORIGINAL SOURCE:
: US-00-060-208-1

```

Query Match	4.1%	Score 73	DB 4	Length 2775
Best Local Similarity	100.0%	Pred. No. 5	Loc-27	
Matches 73	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY 1	AGCTGGAGCTCCACGGCGGTGGCGGGCTCTAAGAACTAGTCGATCCCGCGCTTGTGAGG	50		
Db 37	AGCTGGAGCTCCACGGCGGTGGCGGGCTCTAAGAACTAGTCGATCCCGCGCTTGTGAGG	50		
QY 61	AATTCGGCAGGAG	73		
Db 97	AATTCGGCAGGAG	109		

```

RESULT 13
US-08-472-934-5
: Sequence 5, Application US/08472934
: Patent No. 5753446
: GENERAL INFORMATION:
: APPLICANT: JOHNSON, GARY L.
: TITLE OF INVENTION: METHOD AND
: TITLE OF INVENTION: RESPONSIVE
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Lahive and Cockfield
: STREET: 60 State Street
: CITY: Boston
: STATE: Massachusetts
: COUNTRY: U.S.A.
: ZIP: 02109
: COMPUTER FEASIBLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible

```

```

1 OPERATING SYSTEM: PC-DOS/MS-DOS
2 SOFTWARE: PatentIn Release #1.0, Version #1.25
3 CURRENT APPLICATION DATA:
4 APPLICATION NUMBER: US/08/472,934
5 FILING DATE: 08-JUN-1995
6 CLASSIFICATION: 435
7 PRIOR APPLICATION DATA:
8 APPLICATION NUMBER: US 08/440,421
9 FILING DATE: 15-MAY-1995
10 PRIOR APPLICATION DATA:
11 APPLICATION NUMBER: 08/354,516
12 FILING DATE: 21-FEB-1995
13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER: US 5,405,941
15 FILING DATE: 15-APR-1993
16 PRIOR APPLICATION DATA:
17 APPLICATION NUMBER: 08/323,460
18 FILING DATE: 14-OCT-1994
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: PCT/US94/11690
21 FILING DATE: 14-OCT-1994
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: PCT/US94/04178
24 FILING DATE: 15-APR-1994
25 ATTORNEY/AGENT INFORMATION:
26 NAME: Giulio A. DeConti, Jr. Esq.
27 REGISTRATION NUMBER: 31,503
28 REFERENCE/DOCKET NUMBER: CFI-004DVC62
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE: (617) 227-7400
31 TELEFAX: (617) 227-5941
32 INFORMATION FOR SEQ ID NO: 5:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 3089 base pairs
35 TYPE: nucleic acid
36 STRANDEDNESS: double
37 TOPOLOGY: linear
38 MOLECULE TYPE: cDNA
39 FEATURE:
40 NAME/KEY: CDS
41 LOCATION: 400..2280
42 US-08-472-934-5

```

	Query Match	4.1%;	Score 73;	DB 1;	Length 3089;
	Best Local Similarity	100.0%;	Pred. No. 5.1e-27;		
	Matches 73;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ACTGAGATCCACCGCGGTGGCGGCGGCTCTATAAATATGATCCCGCGGCTGCAGG	60		
DB	11	ACTGAGATCCACCGAGGTGGCGGCGGCTCTATAAATATGATCCCGCGGCTGCAGG	70		
QY	61	AATTCGGCACGAG	73		
DB	71	AATTCGGCACGAG	83		

RESULT 14
US-08-323-460A-5
; Sequence 5, Application US/08323460A
; Patent No. 5854043
; GENERAL INFORMATION:
; APPLICANT: JOHNSON, GARY L.
; TITLE OF INVENTION: METHOD AND PRODUCT FOR PERCUSSING CELL
; TITLE OF INVENTION: RESPONSIVENESS TO EXTERNAL SIGNALS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SHERIDAN ROSS & MCINTOSH
; STREET: 1700 LINCOLN STREET, SUITE 3500
; CITY: DENVER
; STATE: CO
; COUNTRY: USA
; ZIP: 80203
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/323,460A
FILING DATE: 14-OCT-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,254
FILING DATE: 14-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOVARIK, JOSEPH E.
REGISTRATION NUMBER: 33,005
REFERENCE/DOCKET NUMBER: 2879-1-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/863-9700
TELEFAX: 303/863-0223
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3089 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 400..2280
US-08-323-460A-5

Query Match
Best Local Similarity: 4.1%; Score 73; DB 2; Length 3089;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCTGGAGCTCCACCGCGGCTGCGGCGCTTAAAGACTAGTGGATCCCGGAGTGGAGG 60
DB 11 ACCTGGAGCTCCACCGCGGCTGCGGCGCTTAAAGACTAGTGGATCCCGGAGTGGAGG 70
QY 61 AATCGGCACGAG 73
DB 71 AATCGGCACGAG 83

RESULT 15
US-08-461-146C-5
Sequence 5, Application US/08461146C
Patent No. 5981265
GENERAL INFORMATION:
APPLICANT: JOHNSON, GARY L.
TITLE OF INVENTION: METHODS FOR REGULATING MEKK PROTEIN ACTIVITY
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive and Cockfield
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,146C
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/354,516
FILING DATE: 21-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/049,254
FILING DATE: 15-APR-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/323,460
FILING DATE: 14-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/11690
FILING DATE: 14-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04178
FILING DATE: 15-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: KARA, Catherine J.
REGISTRATION NUMBER: P41,106
REFERENCE/DOCKET NUMBER: CPI-004CNS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3089 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 400..2280
US-08-461-146C-5

Query Match
Best Local Similarity: 4.1%; Score 73; DB 2; Length 3089;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCTGGAGCTCCACCGCGGCTGCGGCGCTTAAAGACTAGTGGATCCCGGAGTGGAGG 60
DB 11 ACCTGGAGCTCCACCGCGGCTGCGGCGCTTAAAGACTAGTGGATCCCGGAGTGGAGG 70
QY 61 AATCGGCACGAG 73
DB 71 AATCGGCACGAG 83

RESULT 16
US-08-461-145C-5
Sequence 5, Application US/08461145C
Patent No. 6074861
GENERAL INFORMATION:
APPLICANT: JOHNSON, GARY L.
TITLE OF INVENTION: NOVEL MEKK PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive and Cockfield, LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:-
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,145C
FILING DATE: 5-JUNE-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,254
FILING DATE: 11-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/323,460
FILING DATE: 14-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/11690

```

; FILING DATE: 14-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04178
; FILING DATE: 15-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/354,516
; FILING DATE: 21-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: P-41,106
; REFERENCE/DOCKET NUMBER: CPI-004CN1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3089 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 400..2280
US-08-461-145C-5

```

```

Query Match      4.1%  Score 73:  DB 3:  Length 3089;
Best Local Similarity 100.0%;  Pred. No. 5.1e-27;
Matches 73;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

```

QY 1 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCCGGGCTGCAGG 60
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 11 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCCGGGCTGCAGG 60

```

```

QY 61 AATTCGGCAGCAG 73
   ||||||||||||
DB 71 AATTCGGCAGCAG 83

```

```

RESULT 17
US-08-628-829-5
; Sequence 9, Application US/08628829A
; Patent No. 633170
; GENERAL INFORMATION:
; APPLICANT: Johnson, Gary L.
; TITLE OF INVENTION: Method And Product For Regulating Cell Responsiveness To External
; FILE REFERENCE: CPI-004VCP3
; CURRENT APPLICATION NUMBER: US/08/628,829A
; CURRENT FILING DATE: 1996-04-05
; EARLIER FILING DATE: 1995-05-15
; EARLIER FILING DATE: 1995-05-15
; EARLIER FILING DATE: 1994-10-14
; EARLIER FILING DATE: 1994-10-14
; EARLIER FILING DATE: 1993-05-15
; EARLIER FILING DATE: 1993-05-15
; EARLIER FILING DATE: 1995-04-24
; EARLIER FILING DATE: 1995-04-24
; EARLIER FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 3089
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (400)..(2277)
US-08-628-829-9

```

```

Query Match      4.1%  Score 73:  DB 4:  Length 3089;
Best Local Similarity 100.0%;  Pred. No. 5.1e-27;
Matches 73;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

```

QY 1 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCCGGGCTGCAGG 60
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 11 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCCGGGCTGCAGG 70
QY 61 AATTCGGCAGCAG 73
   ||||||||||||
DB 71 AATTCGGCAGCAG 83

```

```

RESULT 18
US-08-960-048-1
; Sequence 1, Application US/08960048C
; Patent No. 6271443
; GENERAL INFORMATION:
; APPLICANT: Stalker, D. et al.
; TITLE OF INVENTION: Plant Cellulose Synthase and Promoter
; FILE REFERENCE: 15621/01/US
; CURRENT APPLICATION NUMBER: US/08/960,048C
; CURRENT FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/029,987
; PRIOR FILING DATE: 1996-10-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3328
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-08-960-048-1

```

```

Query Match      4.1%  Score 73:  DB 4:  Length 3328;
Best Local Similarity 100.0%;  Pred. No. 5.1e-27;
Matches 73;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

```

QY 1 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCCGGGCTGCAGG 60
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 10 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCCGGGCTGCAGG 99
QY 61 AATTCGGCAGCAG 73
   ||||||||||||
DB 90 AATTCGGCAGCAG 102

```

```

RESULT 19
US-08-795-088A-1
; Sequence 1, Application US/08795088A
; Patent No. 6242569
; GENERAL INFORMATION:
; APPLICANT: Sul, Hong-Bing
; APPLICANT: Goeddel, David V.
; TITLE OF INVENTION: Regulators of Apoptosis
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Science & Technology Law Group
; STREET: 75 Denise Drive
; CITY: Hillsborough
; STATE: California
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-POS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,088A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A

```



```

1 REGISTRATION NUMBER: 36,627
2 REFERENCE/DOCKET NUMBER: 197-001
3 TELECOMMUNICATION INFORMATION:
4 TELEPHONE: (650) 343-4341
5 TELEFAX: (650) 343-4342
6 INFORMATION FOR SEQ. ID NO: 1:
7 SEQUENCE CHARACTERISTICS:
8 LENGTH: 2045 base pairs
9 TYPE: nucleic acid
10 STRANDEDNESS: double
11 TOPOLOGY: linear
12 MOLECULE TYPE: cDNA
13
14 US-08-795-086A-1

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Query Match	4.0%	Score 71	DB 4	Length 2045
Best Local Similarity	100.0%	Pred. No.	5.1e-26	
Matches 71	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY	3	CTGAGAGCTCCACCGCGGGTGGCGGCGCGCTCTACAACTAATGATGATCCCGCGGGCTGCGAGGAA	62
Db	10	CTGAGAGCTCCACCGCGGGTGGCGGCGCGCTCTACAACTAATGATGATCCCGCGGGCTGCGAGGAA	69
QY	63	TTGCGCACGAG 73	
Db	70	TTGCGCACGAG 80	

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1 RESULT 20
2 US-08-668-128B-7
3 : Sequence 7, Application US/08668:28B
4 : Patent No. 5840568
5 :
6 : GENERAL INFORMATION:
7 : APPLICANT: Pfeleudschuh, Michael
8 : TITLE OF INVENTION: Hodgkin's Disease Associated Molecules And
9 : TITLE OF INVENTION: Uses Thereof
10 : NUMBER OF SEQUENCES: 14
11 : CORRESPONDENCE ADDRESS:
12 : ADDRESSEE: Felfe & Lynch
13 : STREET: 805 Third Avenue
14 : CITY: New York City
15 : STATE: New York
16 : ZIP: 10022
17 :
18 : COMPUTER READABLE FORM.
19 : MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
20 : COMPUTER: IBM
21 : OPERATING SYSTEM: PC-DOS
22 : SOFTWARE: Wordperfect
23 : CURRENT APPLICATION DATA:
24 : APPLICATION NUMBER: US/08/668,128B
25 : FILING DATE: 21-JUNE-1996
26 :
27 : CLASSIFICATION: 435
28 : PRIOR APPLICATION DATA:
29 : APPLICATION NUMBER: 08/644,116
30 : FILING DATE: 10-MAY-1996
31 : PRIOR APPLICATION DATA:
32 : APPLICATION NUMBER: 08/580,980
33 : FILING DATE: 03-JANUARY-1996
34 : PRIOR APPLICATION DATA:
35 : APPLICATION NUMBER: 08/479,328
36 : FILING DATE: 07-JUNE-1995
37 : ATTORNEY/AGENT INFORMATION:
38 : NAME: Hanson, No. 5840568man D.
39 : REGISTRATION NUMBER: 30,946
40 : REFERENCE/DOCKET INFORMATION:
41 : TELECOMMUNICATION INFORMATION:
42 : TELEPHONE: (212) 688-9200
43 : TELEFAX: (212) 836-3884
44 : INFORMATION FOR SEQ ID NO: 7:
45 : SEQUENCE CHARACTERISTICS:
46 : LENGTH: 2085 base pairs
47 : TYPE: nucleic acid
48 : STRANDEDNESS: single
49 : TOPOLOGY: linear
50 :

```

```

OS-08-668-128b-7
Query Match          3.9%; Score 70; DB 2; Length 2085;
Best Local Similarity 100.0%; Pred. No. 1.6e-25;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

```

O7	5	GGAAGCTCACAACCCGCGGGGAGGAGCTTAAAGACTGTATCATCTCTTGCGGCTGCAGGAAATT	64
D8	1	GGAGCTCTCAACCGGAGGAGGCGGAGGCTAAGAAATGTAGTGGATTCGCCCGGAGCTGCAGGAAATT	60
O7			
O7	65	CGGCGAGGAGC	74
D8	61	CGGCGAGGAGC	70

RESULT 21
US-08-905-445-7
Sequence 7: Application US/08905445

```

1 GENERAL INFORMATION:
2 APPLICANT: Pfeundsichub, Michael
3 TITLE OF INVENTION: Hodgkin's Disease Associated Molecules And
4 TITLE OF INVENTION: Uses Thereof
5 NUMBER OF SEQUENCES: 14
6 CORRESPONDENCE ADDRESS:
7 ADDRESSEE: Felle & Lynch
8 STREET: 805 Third Avenue
9 CITY: New York City
10 STATE: New York
11 ZIP: 10022
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
14 COMPUTER: IBM
15 OPERATING SYSTEM: PC-DOS
16 SOFTWARE: wordperfect
17 CURRENT APPLICATION DATA:
18 APPLICATION NUMBER: US/08/905,445
19 FILING DATE: 04-AUG-1997
20 CLASSIFICATION: 424
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: 08/668,128
23 FILING DATE: 21-JUNE-1996
24 APPLICATION NUMBER: 08/644,116
25 FILING DATE: 10-MAY-1996
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: 08/580,980
28 FILING DATE: 03-JANUARY-1996
29 PRIOR APPLICATION DATA:
30 APPLICATION NUMBER: 08/479,328
31 FILING DATE: 07-JUNE-1995
32 ATTORNEY/AGENT INFORMATION:
33 NAME: Hanson, No. 5864015man D.
34 REGISTRATION NUMBER: 30,946
35 REFERENCE/DOCKET NUMBER: LUD 5441
36 TELECOMMUNICATION INFORMATION:
37 TELEPHONE: (212) 688-9200
38 TELEFAX: (212) 838-3984
39 INFORMATION FOR SEQ ID NO: 7:
40 SEQUENCE CHARACTERISTICS:
41 LENGTH: 2085 base pairs
42 TYPE: nucleic acid
43 STRANDEDNESS: single
44 TOPOLOGY: linear
45
46 US-08-905-445-7
47
48 Query Match 3.9% Score 70; DB 2; Length 2085;
49 Best Local Similarity 100.0% Pred. No. 1.ee-25;
50 Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
51
52 5 GGAAGCTCCACCGCGGAGTGGCGGCTCTGTGAACCTAATGAGATCCCGCGGCTGCAGGAATT 64
53 |||||||
54 1 GGAGCTCCACCGCGGAGTGGCGGCTCTGTGAACCTAATGAGATCCCGCGGCTGCAGGAATT 60

```

QY 5 GAGAGCTCCACCGGCGGTGGCGGCGGCTTAGAAGTCTAGTGATCCCCGGGAGTCAGGAATT 64
|||||
|||
Db 1 GAGAGCTCCACCGGCGGTGGCGGCGGCTTAGAAGTCTAGTGATCCCCGGGAGTCAGGAATT 60

QY 65 CGCAGCAGC 74
 |||||
 Db 61 CGCAGCAGC 70

RESULT 22

US-08-818-112-101/c
 : Sequence 101, Application US/08818112
 : Patent No. 6290969
 : GENERAL INFORMATION:
 : APPLICANT: Reed, Steven G.
 : APPLICANT: Skeiky, Yasir A.W.
 : APPLICANT: Dillon, Davin C.
 : APPLICANT: Campos-Neto, Antonio
 : APPLICANT: Houghton, Raymond
 : APPLICANT: Vedvick, Thomas S.
 : APPLICANT: Twardzik, Daniel R.
 : TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
 : TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
 : NUMBER OF SEQUENCES: 153
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: SEED and BERRY LLP
 : STREET: 6300 Columbia Center, 701 Fifth Avenue
 : CITY: Seattle
 : STATE: Washington
 : COUNTRY: USA
 : ZIP: 98104-7092
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/818,112
 : FILING DATE: 13-MAR-1997
 : CLASSIFICATION: 424
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Maki, David J.
 : REGISTRATION NUMBER: 31,392
 : REFERENCE/DOCKET NUMBER: 210121.411C6
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (206) 622-4900
 : TELEFAX: (206) 682-6031
 : INFORMATION FOR SEQ ID NO: 101:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 500 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : US-08-818-112-101

Query Match 3.8%; Score 67; DB 4; Length 500;
 Best Local Similarity 100.0%; Pred. No. 5.3e-24;
 Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AGCTCCACCGCGTGGCGCGCTCTAGAACTAGTGGATCCCGCGCTGCAGGAATTCG 66
 |||||
 Db 500 AGCTCCACCGCGTGGCGCGCTCTAGAACTAGTGGATCCCGCGCTGCAGGAATTCG 441

QY 67 GCACGAG 73
 |||||
 Db 440 GCACGAG 434

RESULT 23

US-08-818-111-96/c
 : Sequence 96, Application US/08818111
 : Patent No. 6338852
 : GENERAL INFORMATION:
 : APPLICANT: Reed, Steven G.
 : APPLICANT: Skeiky, Yasir A.W.
 : APPLICANT: Dillon, Davin C.
 : APPLICANT: Campos-Neto, Antonio

APPLICANT: Houghton, Raymond
 APPLICANT: Vedvick, Thomas S.
 APPLICANT: Twardzik, Daniel R.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TUBERCULOSIS
 NUMBER OF SEQUENCES: 148
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/818,111
 FILING DATE: 13-MAR-1997
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.417C6
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 96:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 500 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-818-111-96

Query Match 3.8%; Score 67; DB 4; Length 500;
 Best Local Similarity 100.0%; Pred. No. 5.3e-24;
 Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AGCTCCACCGCGTGGCGCGCTCTAGAACTAGTGGATCCCGCGCTGCAGGAATTCG 66
 |||||
 Db 500 AGCTCCACCGCGTGGCGCGCTCTAGAACTAGTGGATCCCGCGCTGCAGGAATTCG 441

QY 67 GCACGAG 73
 |||||
 Db 440 GCACGAG 434

RESULT 24

US-09-056-556-101/c
 : Sequence 101, Application US/09056556
 : Patent No. 6350456
 : GENERAL INFORMATION:

APPLICANT: Reed, Steven G.
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Dillon, Davin C.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND
 NUMBER OF SEQUENCES: 241
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/056,556

TRE

FILING DATE: 07-APR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 623-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 500 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-036-556-101

Query Match 3.8%; Score 67; DB 4; Length 500;
Best Local Similarity 100.0%; Pred. No. 5.3e-24;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AGCTCACCAGCGGTGGCGCGCTAGACTAGTGCATCCCGCGGCTGCAGGAATTCG 66
|||||
DB 500 AGCTCACCAGCGGTGGCGCGCTAGACTAGTGCATCCCGCGGCTGCAGGAATTCG 441

QY 67 GCACGAG 73
|||||
DB 440 GCACGAG 434

RESULT 25
US-09-072-596-96/c
Sequence 96, Application US/09072596
Patent No. 6458366
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, David C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vedgick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodges, Michael J.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and HERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 623-6031
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 500 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
US-09-072-596-96

Query Match 3.8%; Score 67; DB 4; Length 500;
Best Local Similarity 100.0%; Pred. No. 5.3e-24;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AGCTCACCAGCGGTGGCGCGCTAGACTAGTGCATCCCGCGGCTGCAGGAATTCG 66
|||||
DB 500 AGCTCACCAGCGGTGGCGCGCTAGACTAGTGCATCCCGCGGCTGCAGGAATTCG 441

QY 67 GCACGAG 73
|||||
DB 440 GCACGAG 434

RESULT 26
US-08-976-259-108/c
Sequence 108, Application US/08976259
Patent No. 6316609
GENERAL INFORMATION:
APPLICANT: Dillon, Patrick J.
APPLICANT: Choi, Gil H.
APPLICANT: Welch, Rodney A.
TITLE OF INVENTION: Nucleotide Sequence of Escherichia coli
Patent No. 6316609
NUMBER OF SEQUENCES: 142
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Ave, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,259
FILING DATE: Herewith
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/031,626 AND US 60/061,953
ATTORNEY/AGENT INFORMATION:
NAME: Steife, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0740002/EKS/CBM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 752 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-976-259-108

Query Match 3.7%; Score 66; DB 4; Length 752;
Best Local Similarity 100.0%; Pred. No. 1.7e-23;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGCTCCACCGCGGTGGCGCGCTAGACTAGTGCATCCCGCGGCTGCAGG 60
|||||
DB 111 AGCTGAGCTCCACCGCGGTGGCGCGCTAGACTAGTGCATCCCGCGGCTGCAGG 52

QY 61 AATTCG 66
|||||
DB 51 AATTCG 46

```
RESULT 27
US-08-646-538-14
; Sequence 14, Application US/08646538
; Patent No. 6027881
; GENERAL INFORMATION:
; APPLICANT: Pavlakis, George N.
; APPLICANT: Gaitanaris, George A.
; APPLICANT: Stauber, Roland H.
; APPLICANT: Vournakis, John N.
; TITLE OF INVENTION: Mutant Aequorea victoria Fluorescent
; TITLE OF INVENTION: Proteins Having Increased Cellular Fluorescence
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: No. 6027881 yet assigned
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 015280-249000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 849 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..849
; OTHER INFORMATION: /note= "pBSGFPsgll"
US-08-646-538-14

Query Match 3.7%; Score 66; DB 3; Length 849;
Best Local Similarity 100.0%; Pred. No. 1.7e-23;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGCGTGGCGCGCTCTAGAACTAGTGGATCCCGCGGTGCAGG 60
Db 52 AGCTGGAGCTCCACCGCGTGGCGCGCTCTAGAACTAGTGGATCCCGCGGTGCAGG 111

QY 61 AATTCG 66
Db 112 AATTCG 117

RESULT 28
US-09-503-222-14
; Sequence 14, Application US/0950222
; Patent No. 6265548
; GENERAL INFORMATION:
; APPLICANT: Pavlakis, George N.
; APPLICANT: Gaitanaris, George A.
; APPLICANT: Stauber, Roland H.
; APPLICANT: Vournakis, John N.
; TITLE OF INVENTION: Mutant Aequorea victoria Fluorescent
; TITLE OF INVENTION: Proteins Having Increased Cellular Fluorescence
```

```
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/09/503/222
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,538
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 015280-249000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 849 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..849
; OTHER INFORMATION: /note= "pBSGFPsgll"
US-09-503-222-14

Query Match 3.7%; Score 66; DB 4; Length 849;
Best Local Similarity 100.0%; Pred. No. 1.7e-23;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGCGTGGCGCGCTCTAGAACTAGTGGATCCCGCGGTGCAGG 60
Db 52 AGCTGGAGCTCCACCGCGTGGCGCGCTCTAGAACTAGTGGATCCCGCGGTGCAGG 111

QY 61 AATTCG 66
Db 112 AATTCG 117

RESULT 29
US-09-424-283-5/c
; Sequence 5, Application US/09424283
; Patent No. 6437219
; GENERAL INFORMATION:
; APPLICANT: Grimes, et al.
; TITLE OF INVENTION: Suctose binding proteins
; FILE REFERENCE: 4630-50206
; CURRENT APPLICATION NUMBER: US/99/424,283
; PRIOR FILING DATE: 1999-11-19
; PPTC APPLICATION NUMBER: PCI/US99/10465
; PRIOR FILING DATE: 1998-05-21
; PRIOR APPLICATION NUMBER: US 60/047,568
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1924
; TYPE: DNA
; ORGANISM: Glycine max
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FEATURE:
NAME/KEY: CDS
LOCATION: (119)..(1588)
US-09-424-283-5

Query Match 3.7% Score 66; DB 4; Length 1924;
Best Local Similarity 100.0%; Pred. No. 1.7e-23;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGCTCCACGGCGGTGGCGCCCTCTAGACTAGTGTATCCCGCGCTGCAGG 60
DB 1881 AGCTGAGCTCCACCGCGGTGGCGCCCTCTAGACTAGTGTATCCCGCGCTGCAGG 1822

QY 61 AATTCG 66
DB 1821 AATTCG 1816

RESULT 30
US-09-215-221-9/c
Sequence 9, Application US/09215221
Patent No. 6265562
GENERAL INFORMATION:
APPLICANT: EILERS, MARTIN
APPLICANT: EBERS, ANDREA
APPLICANT: SEDLACEK, HANS-HARALD
TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY
TITLE OF INVENTION: INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF
FILE REFERENCE: 026083/0192
CURRENT APPLICATION NUMBER: US/09/215,221
CURRENT FILING DATE: 1998-12-18
PRIOR FILING DATE: 1997-12-20
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 1958
TYPE: DNA
ORGANISM: Murine sp.
US-09-215-221-9

Query Match 3.7% Score 66; DB 4; Length 1958;
Best Local Similarity 100.0%; Pred. No. 1.7e-23;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGCTCCACCGCGGTGGCGCCCTCTAGAACTAGTGTATCCCGCGCTGCAGG 60
DB 1949 AGCTGAGCTCCACCGCGGTGGCGCCCTCTAGAACTAGTGTATCCCGCGCTGCAGG 1890

QY 61 AATTCG 66
DB 1889 AATTCG 1884

RESULT 31
US-08-446-935-6/c
Sequence 6, Application US/08446935
Patent No. 6187991
GENERAL INFORMATION:
APPLICANT: Soeller, Walter C.
APPLICANT: Carly, Maynard D.
APPLICANT: Kreutler, David K.
TITLE OF INVENTION: TRANSGENIC ANIMAL MODELS FOR TYPE 1
TITLE OF INVENTION: DIABETES MELLITUS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pfizer Inc.
STREET: 235 East 42nd Street, 20th Floor
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10017-5755
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,935
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sheyfa, Robert F.
REGISTRATION NUMBER: 31,304
REFERENCE/DOCKET NUMBER: PC8153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)573-1189
TELEFAX: (212)573-1939
TELEX: N/A
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2961 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
US-08-446-935-6

Query Match 3.7% Score 66; DB 4; Length 2961;
Best Local Similarity 100.0%; Pred. No. 1.7e-23;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGCTCCACCGCGGTGGCGCCCTCTAGAACTAGTGTATCCCGCGCTGCAGG 60
DB 765 AGCTGAGCTCCACCGCGGTGGCGCCCTCTAGAACTAGTGTATCCCGCGCTGCAGG 706

QY 61 AATTCG 66
DB 705 AATTCG 700

RESULT 32
US-08-646-538-6/c
Sequence 6, Application US/08646538
Patent No. 6027881
GENERAL INFORMATION:
APPLICANT: Pavlakis, George N.
APPLICANT: Galtanakis, George A.
APPLICANT: Stauber, Roland H.
APPLICANT: Vournakis, John N.
TITLE OF INVENTION: Mutant Aequorea victoria Fluorescent
TITLE OF INVENTION: Proteins Having Increased Cellular Fluorescence
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,538
FILING DATE: No. 6027881 yet assigned
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 015280-249000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

```

; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 3699 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA
;   FEATURE:
;     NAME/KEY: -
;     LOCATION: 1..3699
;     OTHER INFORMATION: /note="pBSGFP"
;
US-08-646-538-6

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Query Match          3.7%; Score 66; DB 3; Length 3699;
Best Local Similarity 100.0%; Pred. No. 1.7e-23;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGGCGGCGGCGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 60
    |||||||
Db 1500 AGCTGGAGCTCCACCGGCGGCGGCGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 1441

QY 61 AATTCG 66
    |||||
Db 1440 AATTCG 1435

```

```

RESULT 33
US-09-503-222-6/c
; Sequence 6, Application US/09503222
; Patent No. 6265548
; GENERAL INFORMATION:
;   APPLICANT: Pavlakis, George N.
;   APPLICANT: Gaitanaris, George A.
;   APPLICANT: Stauber, Roland H.
;   APPLICANT: Vournakis, John N.
;   TITLE OF INVENTION: Mutant Aequorea victoria Fluorescent
;   TITLE OF INVENTION: Proteins Having Increased Cellular Fluorescence
;   NUMBER OF SEQUENCES: 37
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Townsend and Townsend and Crew LLP
;     STREET: Two Embarcadero Center, 8th Floor
;     CITY: San Francisco
;     STATE: California
;     COUNTRY: USA
;     ZIP: 94111-3834
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/503,222
;     FILING DATE:
;     CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       PRIOR APPLICATION NUMBER: US/08/646,538
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME: Weber, Kenneth A.
;       REGISTRATION NUMBER: 31,677
;       REFERENCE/DOCKET NUMBER: 015280-249000
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (415) 576-0200
;       TELEFAX: (415) 576-0300
;     INFORMATION FOR SEQ ID NO: 6:
;       SEQUENCE CHARACTERISTICS:
;         LENGTH: 3699 base pairs
;         TYPE: nucleic acid
;         STRANDEDNESS: single
;         TOPOLOGY: linear
;         MOLECULE TYPE: DNA
;         FEATURE:
;           NAME/KEY: -

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; LOCATION: 1..3699
; OTHER INFORMATION: /note="pBSGFP"
;
US-09-503-222-6
;
Query Match          3.7%; Score 66; DB 4; Length 3699;
Best Local Similarity 100.0%; Pred. No. 1.7e-23;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGGCGGCGGCGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 60
    |||||||
Db 1500 AGCTGGAGCTCCACCGGCGGCGGCGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 1441

QY 61 AATTCG 66
    |||||
Db 1440 AATTCG 1435

RESULT 34
US-08-992-334-1/c
; Sequence 1, Application US/08992334
; Patent No. 5919678
; GENERAL INFORMATION:
;   APPLICANT: Gruss, Alexandra
;   APPLICANT: Maguin, Emmanuelle
;   TITLE OF INVENTION: METHODS FOR USING A TEMPERATURE-SENSITIVE
;   TITLE OF INVENTION: PLASMID
;   NUMBER OF SEQUENCES: 3
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Christie Parker & Hale, LLP
;     STREET: 350 West Colorado Boulevard, Suite 500
;     CITY: Pasadena
;     STATE: California
;     COUNTRY: United States
;     ZIP: 91105
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/992,334
;     FILING DATE: 17-DEC-1997
;     CLASSIFICATION: 435
;     PRIOR APPLICATION DATA:
;       PRIOR APPLICATION NUMBER: US 08/302,752
;       FILING DATE: 24-DEC-1994
;     PRICE APPLICATION DATA:
;       APPLICATION NUMBER: PCT/FR93/00248
;       FILING DATE: 12-MAR-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: FR 992/03034
;       FILING DATE: 13-MAR-1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME: Prout, D. Bruce
;       REGISTRATION NUMBER: 20958
;       REFERENCE/DOCKET NUMBER: C93:31779
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (626) 795-9900
;       TELEFAX: (626) 577-8800
;     INFORMATION FOR SEQ ID NO: 1:
;       SEQUENCE CHARACTERISTICS:
;         LENGTH: 3792 base pairs
;         TYPE: nucleic acid
;         STRANDEDNESS: both
;         TOPOLOGY: circular
;         MOLECULE TYPE: DNA (genomic)
;         HYPOTHETICAL: NO
;         ANTI-SENSE: YES
;         IMMEDIATE SOURCE:
;           CLONE: pg+host4
;
US-08-992-334-1

```

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Query Match          3.7%; Score 66; DB 2; Length 3792;

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Best Local Similarity 100.0%; Pred. No. 1.7e-23;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTATCGGCGGCGGCTGAGG 60
|||||
Db 3580 AGCTGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTATCGGCGGCGGCTGAGG 3521

QY 61 AATTCG 66
|||||
Db 3520 AATTCG 3515

RESULT 35
US-08-302-752-1/c
Sequence 1, Application US/08302752
Patent No. 6025190

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: THERMOSENSIBLE PLASMID

NUMBER OF SEQUENCES: 3

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/302,752

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 9203034

FILING DATE: 13-MAR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO FR/93/00248

FILING DATE: 12-MAR-1993

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3792 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-302-752-1

Query Match
Best Local Similarity 100.0%; Pred. No. 1.7e-23;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTATCGGCGGCGGCTGAGG 60
|||||
Db 3580 AGCTGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTATCGGCGGCGGCTGAGG 3521

QY 61 AATTCG 66
|||||
Db 3520 AATTCG 3515

RESULT 36
US-08-992-334-2/c
Sequence 2, Application US/08992334
Patent No. 5919678

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: THERMOSENSIBLE PLASMID

NUMBER OF SEQUENCES: 3

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/302,752

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 9203034

FILING DATE: 13-MAR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO FR/93/00248

FILING DATE: 12-MAR-1993

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 5234 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: circular

ZIP: 91105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/992,334

FILING DATE: 17-DEC-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/302,752

FILING DATE: 24-DEC-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/FR93/00248

FILING DATE: 12-MAR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR FR92/03034

FILING DATE: 13-MAR-1992

ATTORNEY/AGENT INFORMATION:

NAME: Prout, D. Bruce

REGISTRATION NUMBER: 20958

REFERENCE/DOCKET NUMBER: G93:31779

TELECOMMUNICATION INFORMATION:

TELEPHONE: (626) 795-9900

TELEFAX: (626) 577-8800

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 5234 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

US-08-992-334-2

Query Match
Best Local Similarity 100.0%; Pred. No. 1.7e-23;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTATCGGCGGCGGCTGAGG 60
|||||
Db 5022 AGCTGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTATCGGCGGCGGCTGAGG 4963

QY 61 AATTCG 66
|||||
Db 4962 AATTCG 4957

RESULT 37
US-08-302-752-2/c
Sequence 2, Application US/08302752
Patent No. 6025190

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: THERMOSENSIBLE PLASMID

NUMBER OF SEQUENCES: 3

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/302,752

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 9203034

FILING DATE: 13-MAR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO FR/93/00248

FILING DATE: 12-MAR-1993

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 5234 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

US-08-992-334-2

LENGTH: 5234 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-302-752-2

Query Match 3.7%; Score 66; DB 3; Length 5234;
Best Local Similarity 100.0%; Pred. No. 1.7e-23;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCTGGAGCTCCACGGGCTGGGCGGCGCTCTAGAACTAGTGGATCCCGGGCTGAGG 60
|||||
Db 5022 AGCTGGAGCTCCACGGGCTGGGCGGCGCTCTAGAACTAGTGGATCCCGGGCTGAGG 60
QY 61 AATTCG 66
|||||
Db 4962 AATTCG 4957

RESULT 38
US-08-675-566-18/c
Sequence 18, Application US/08675566
Patent No. 6090393
GENERAL INFORMATION:
APPLICANT: Fischer, Laurent
TITLE OF INVENTION: PROMOTERS, EXPRESSION CASSETTES,
TITLE OF INVENTION: RECOMBINANT VIRUSES, METHODS FOR MAKING, AND USES THEREOF
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford, P.C.
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,566
FILING DATE: 03-JUL-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Frommer Esq., William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2890
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)840-3333
TELEFAX: (212)840-0712
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 6045 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-675-566-18

Query Match 3.7%; Score 66; DB 3; Length 6045;
Best Local Similarity 100.0%; Pred. No. 1.7e-23;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCTGGAGCTCCACGGGCTGGGCGGCGCTCTAGAACTAGTGGATCCCGGGCTGAGG 60
|||||
Db 3159 AGCTGGAGCTCCACGGGCTGGGCGGCGCTCTAGAACTAGTGGATCCCGGGCTGAGG 60
QY 61 AATTCG 66
|||||
Db 3099 AATTCG 3094

Query Match 3.7%; Score 66; DB 3; Length 6045;
Best Local Similarity 100.0%; Pred. No. 1.7e-23;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCTGGAGCTCCACGGGCTGGGCGGCGCTCTAGAACTAGTGGATCCCGGGCTGAGG 60
|||||
Db 3159 AGCTGGAGCTCCACGGGCTGGGCGGCGCTCTAGAACTAGTGGATCCCGGGCTGAGG 60
QY 61 AATTCG 66
|||||
Db 3099 AATTCG 3094

RESULT 39

US-08-675-566-17/c
Sequence 17, Application US/08675566
Patent No. 6090393
GENERAL INFORMATION:

APPLICANT: Fischer, Laurent
TITLE OF INVENTION: PROMOTERS, EXPRESSION CASSETTES,
TITLE OF INVENTION: RECOMBINANT VIRUSES, METHODS FOR MAKING, AND USES THEREOF
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford, P.C.
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,566
FILING DATE: 03-JUL-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Frommer Esq., William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2890
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)840-3333
TELEFAX: (212)840-0712
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 6244 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-675-566-17

Query Match

Best Local Similarity 100.0%; Pred. No. 1.7e-23;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACGGGCTGGGCGGCGCTCTAGAACTAGTGGATCCCGGGCTGAGG 60
|||||
Db 3358 AGCTGGAGCTCCACGGGCTGGGCGGCGCTCTAGAACTAGTGGATCCCGGGCTGAGG 60
QY 61 AATTCG 66
|||||
Db 3298 AATTCG 3293

RESULT 40

US-08-675-566-16/c
Sequence 16, Application US/08675566
Patent No. 6090393
GENERAL INFORMATION:

APPLICANT: Fischer, Laurent
TITLE OF INVENTION: PROMOTERS, EXPRESSION CASSETTES,
TITLE OF INVENTION: RECOMBINANT VIRUSES, METHODS FOR MAKING, AND USES THEREOF
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford, P.C.
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/675,566
 FILING DATE: 03-JUL-1996
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Frommer Esq., William S.
 REGISTRATION NUMBER: 25,506
 REFERENCE/DOCKET NUMBER: 454310-2890
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212)840-3333
 TELEFAX: (212)840-0712
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6447 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-675-566-16

Query Match 3.7% Score 66; DB 3; Length 6447;
 Best Local Similarity 100.0%; Pred. No. 1.7e-23;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGCTCCACCGCGGTGGCGCGCTCTAGAACTAGTGTGATCCCGCGGCTGCAGG 60
 DB 3561 AGCTGAGCTCCACCGCGGTGGCGCGCTCTAGAACTAGTGTGATCCCGCGGCTGCAGG 3502
 QY 61 AATTCG 66
 DB 3501 AATTCG 3496

RESULT 41
 US-08-675-566-4/c
 Sequence 4, Application US/08675566
 Patent No. 6090393
 GENERAL INFORMATION:
 APPLICANT: Fischer, Laurent
 TITLE OF INVENTION: PROMOTERS, EXPRESSION CASSETTES,
 TITLE OF INVENTION: RECOMBINANT VIRUSES, METHODS FOR MAKING, AND USES THEREOF
 NUMBER OF SEQUENCES: 120
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Curtis, Morris & Safford, P.C.
 STREET: 530 Fifth Avenue
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/675,566
 FILING DATE: 03-JUL-1996
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Frommer Esq., William S.
 REGISTRATION NUMBER: 25,506
 REFERENCE/DOCKET NUMBER: 454310-2890
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212)840-3333
 TELEFAX: (212)840-0712
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6578 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single

TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-675-566-4
 Query Match 3.7% Score 66; DB 3; Length 6578;
 Best Local Similarity 100.0%; Pred. No. 1.7e-23;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGCTCCACCGCGGTGGCGCGCTCTAGAACTAGTGTGATCCCGCGGCTGCAGG 60
 DB 4516 AGCTGAGCTCCACCGCGGTGGCGCGCTCTAGAACTAGTGTGATCCCGCGGCTGCAGG 4457
 QY 61 AATTCG 66
 DB 4456 AATTCG 4451

RESULT 42
 US-08-675-566-15/c
 Sequence 15, Application US/08675566
 Patent No. 6090393
 GENERAL INFORMATION:
 APPLICANT: Fischer, Laurent
 TITLE OF INVENTION: PROMOTERS, EXPRESSION CASSETTES,
 TITLE OF INVENTION: RECOMBINANT VIRUSES, METHODS FOR MAKING, AND USES THEREOF
 NUMBER OF SEQUENCES: 120
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Curtis, Morris & Safford, P.C.
 STREET: 530 Fifth Avenue
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/675,566
 FILING DATE: 03-JUL-1996
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Frommer Esq., William S.
 REGISTRATION NUMBER: 25,506
 REFERENCE/DOCKET NUMBER: 454310-2890
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212)840-3333
 TELEFAX: (212)840-0712
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6612 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-675-566-15

Query Match 3.7% Score 66; DB 3; Length 6612;
 Best Local Similarity 100.0%; Pred. No. 1.7e-23;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGCTCCACCGCGGTGGCGCGCTCTAGAACTAGTGTGATCCCGCGGCTGCAGG 60
 DB 3726 AGCTGAGCTCCACCGCGGTGGCGCGCTCTAGAACTAGTGTGATCCCGCGGCTGCAGG 3667
 QY 61 AATTCG 66
 DB 3666 AATTCG 3661

RESULT 43
 US-08-992-334-3/c

Sequence 3, Application US/08992334
Patent No. 5919678
GENERAL INFORMATION:
APPLICANT: Gruss, Alexandra
APPLICANT: Maguin, Emmanuelle
TITLE OF INVENTION: METHODS FOR USING A TEMPERATURE-SENSITIVE
TITLE OF INVENTION: PLASMID
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christie Parker & Hale, LLP
STREET: 350 West Colorado Boulevard, Suite 500
CITY: Pasadena
STATE: California
COUNTRY: United States
ZIP: 91105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/992,334
FILING DATE: 17-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/302,752
FILING DATE: 24-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR93/00248
FILING DATE: 12-MAR-1993
APPLICATION NUMBER: FR 992/03034
FILING DATE: 13-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Prout, D. Bruce
REGISTRATION NUMBER: 20958
REFERENCE/DOCKET NUMBER: C93:31779
TELEPHONE: (626) 795-9900
TELEFAX: (626) 577-8800
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6722 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
US-08-992-334-3

Query Match 3.7%, Score 66; DB 2; Length 6722;
Best Local Similarity 100.0%; Pred. No. 1.7e-23;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGGCGTGGGCGGCTCTAGAACTAGTGGATCCCGGGGTGGAGG 60
|||||
Db 6510 AGCTGGAGCTCCACCGGCGTGGGCGGCTCTAGAACTAGTGGATCCCGGGGTGGAGG 60
|||||

QY 61 AATTCG 66
|||||
Db 6450 AATTCG 6445

RESULT 44
US-08-402-752-3/C
Sequence 3, Application US/08302752
Patent No. 6025190
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: THERMOSENSIBLE PLASMID
NUMBER OF SEQUENCES: 3
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/302,752
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9203034
FILING DATE: 13-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO FR/93/00248
FILING DATE: 12-MAR-1993
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6722 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-302-752-3

Query Match 3.7%, Score 66; DB 3; Length 6722;
Best Local Similarity 100.0%; Pred. No. 1.7e-23;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATTCGATCCACCGGCGTGGGCGGCTCTAGAACTAGTGGATCCCGGGGTGGAGG 60
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Db 6510 AGCTGGAGCTCCACCGGCGGCGGCTCTAGAACTAGTGGATCCCGGGGTGGAGG 60
|||||

QY 61 AATTCG 66
|||||
Db 6450 AATTCG 6445

RESULT 45
US-08-675-566-2/C
Sequence 2, Application US/08675566
Patent No. 6090393
GENERAL INFORMATION:
APPLICANT: Fischer, Laurent
TITLE OF INVENTION: PROMOTERS, EXPRESSION CASSETTES,
TITLE OF INVENTION: RECOMBINANT VIRUSES, METHODS FOR MAKING, AND USES THEREOF
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford, P.C.
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,566
FILING DATE: 03-JUL-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Frommer Esq., William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2890
TELEPHONE: (212)840-3333
TELEFAX: (212)840-0712
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6958 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)


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1 CLASSIFICATION: 435
2 ATTORNEY/AGENT INFORMATION:
3 NAME: Seay, Nicholas J
4 REGISTRATION NUMBER: 27386
5 REFERENCE/POCKET NUMBER: 110229.91144
6 TELECOMMUNICATION INFORMATION:
7 TELEPHONE: 608-251-5000
8 TELEFAX: 608-251-9166
9 INFORMATION FOR SEQ ID NO: 1:
10 SEQUENCE CHARACTERISTICS:
11 LENGTH: 7287 base pairs
12 TYPE: nucleic acid
13 STRANDEDNESS: double
14 TOPOLOGY: circular
15 MOLECULE TYPE: other nucleic acid
16 DESCRIPTION: /desc = "plasmid DNA"
17 IMMEDIATE SOURCE:
18 CLONE: pWRG3169
19 FEATURE:
20 NAME/KEY: promoter
21 LOCATION: 1..628
22 FEATURE:
23 NAME/KEY: IDNA
24 LOCATION: 629..810
25 FEATURE:
26 NAME/KEY: CDS
27 LOCATION: join(953..1258, 1332..1673)
28 OTHER INFORMATION: /product= "p35 gene product"
29 FEATURE:
30 NAME/KEY: polyA_site
31 LOCATION: 1797..2024
32 FEATURE:
33 NAME/KEY: promoter
34 LOCATION: 2110..2737
35 FEATURE:
36 NAME/KEY: IDNA
37 LOCATION: 2738..2913
38 FEATURE:
39 NAME/KEY: CDS
40 LOCATION: 2983..3990
41 OTHER INFORMATION: /product= "p40 gene product"
42 FEATURE:
43 NAME/KEY: polyA_site
44 LOCATION: 4075..4306
45 PS-08-659-206A-1

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Query Match      3.7%; Score 66; DB 2; Length 7267;
Best Local Similarity 100.0%; Pred. No. 1.7e-23;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGACTCAGCGGCTGGCGGCGCTTTAAGAACTATGATGATCGGCGGCTGAGG 60
    |||||
DB 7202 AGCTGGACTCAGCGGCTGGCGGCGCTTTAAGAACTATGATGATCGGCGGCTGAGG 7261

QY 61 AATTGG 66
    |||||
DB 7262 AATTGG 7267

```

RESULT 49
US-08-818-112-14
; Sequence 14, Application US/08818112
; Patent No. 6290969
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Houghton, Raymond
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Twardzik, Daniel R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS

NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMREF: 210121, 411C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1058 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-C8-818-112-14

Query Match 3.7%; Score 65; DB 4; Length 1058;
Best Local Similarity 100.0%, Fred. No. 5,3e+23,
Matches 65, Conservative 0; Mismatches 0, Indels 0, Gaps 0;

QY	9	CTCCACCGGCGTGGCGCGCGCTATTAGAAATTAGTAGTAGATATCCCTGGGCTGCAGGAATTCGGC	68
Db	1	CTCCACCGCGGTGGCGCGCGCTATTAGAAATTAGTAGTAGATATCCCTGGGCTGCAGGAATTCGGC	60
QY	69	ACGAG 73	
Db	61	ACGAG 65	

RESULT 50
US-08-818-11-14
Sequence 11, Application US/08018111
Patent No. 6338952
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Lullion, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedwicz, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOSITES AND
NUMBER OF SEQUENCES: 148

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1  TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TUBERCULOSIS
2
3  NUMBER OF SEQUENCES: 148
4  CORRESPONDENCE ADDRESS:
5  ADDRESSEE: SEED and BERRY LLP
6  STREET: 6300 Columbia Center, 701 Fifth Avenue
7  CITY: Seattle
8  STATE: Washington
9  COUNTRY: USA
10 ZIP: 98104-7092
11
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: Floppy disk
14 COMPUTER: IBM PC compatible
15 OPERATING SYSTEM: PC-DOS/MS-DOS
16 SOFTWARE: PatentIn Release #1.0, Version #1.30
17 CURRENT APPLICATION DATA:
18 APPLICATION NUMBER: US/08/818.111

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